

STIC-Biotech/ChemLib

From: Whiteman, Brian
Sent: Monday, April 28, 2003 10:43 AM
To: STIC-Biotech/ChemLib
Subject: seq search

09/818,943 3/28/01
Eriksson et al.

search seq id nos: 1 and 2 against us patent and us patent application databases.

Claiming a transgenic mouse comprising a nucleotide encoding either seq id no: 1 or 2.

Thanks,
Brian Whiteman, 11e12
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
Crystal Mall 1, 11A16
(703) 305-0775

Point of Contact:
Toby Port
Technical Info. Specialist
CRM1 6A04
703-302-2534

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 4/29
Date Completed: 4/29
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:04:36 ; Search time 12.5 seconds

(Without alignments)
812.073 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858

Sequence: 1 MSLEGLLVTSALAGORRGT.....DVALEHHECDVCVCGSTGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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26: /cgn2_6/ptodata/1/1aa/6W.COMB.pep:*

27: /cgn2_6/ptodata/1/1aa/6X.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
4	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
5	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
6	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
7	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
8	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
9	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
10	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
11	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
12	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
13	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
14	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
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19	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
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21	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
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23	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
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26	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl
27	1851	99.6	345	US-09-040-220D-2	Sequence 2, Appl

28	149	8.0	591	3	US-08-991-408-4	Sequence 4, Appl
29	149	8.0	591	4	US-09-432-473-4	Sequence 5, Appl
30	149	8.0	1013	2	US-08-866-650-5	Sequence 4, Appl
31	149	8.0	1013	3	US-09-021-287-5	Sequence 5, Appl
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34	149	8.0	1013	4	US-09-432-473-2	Sequence 3, Appl
35	148	8.0	1013	2	US-08-866-650-3	Sequence 2, Appl
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38	147	7.9	354	4	US-08-915-795-5	Sequence 5, Appl
39	142	7.6	325	4	US-08-915-795-3	Sequence 3, Appl
40	140	7.5	103	4	US-09-374-135-5	Sequence 3, Appl
41	140	7.5	321	4	US-08-915-795-9	Sequence 9, Appl
42	140	7.5	358	4	US-08-915-795-8	Sequence 8, Appl
43	132	7.1	419	2	US-09-374-135-8	Sequence 8, Appl
44	132	7.1	419	2	US-08-999-811-2	Sequence 2, Appl
45	132	7.1	419	3	US-09-042-105-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-040-220D-2
Sequence 2, Application US/09040220D
Patent No. 6391311
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
FILE REFERENCE: P1122
CURRENT APPLICATION NUMBER: US/09/040,220D
CURRENT FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Human
US-09-040-220D-2

Query Match 99.6% Score 1851; DB 4; Length 345;
Best Local Similarity 99.4% Pred. No. 4.8e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MSLEGLLVTSALAGORRGTQAESNLSSKRFQSSNKQNGVODPQHERLITVSTNGSIHS 60
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DB 61 PREPHTYPRNTVLVWRLVAEEVNWVQLTFDERFGLDEPDDICKYDFVEVERPSDGTLL 120
QY 121 GRWCGGTVPGRKQISGNQIRIFRVSDEVPSPGCHINYIMVQFTEAVSVLPSPA 180
DB 121 GRWCGGTVPGRKQISGNQIRIFRVSDEVPSPGCHINYIMVQFTEAVSVLPSPA 180
QY 181 LPDLNNAITAFSTEDLIRYLEPERMOLDLRLPTWOLGKAFVGRKSRVVDLNL 240
DB 181 LPDLNNAITAFSTEDLIRYLEPERMOLDLRLPTWOLGKAFVGRKSRVVDLNL 240
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DB 241 LVEEVLVLCSTPRNFSVSIREELKRTDTLFWPGCLLVKRCGGACCLHNCNCCQVPSK 300
QY 301 VTKKYEVLQLRPKTGVGRGLHSKLTQVLALEHHECDVCVCGSTGG 345
DB 301 VTKKYEVLQLRPKTGVGRGLHSKLTQVLALEHHECDVCVCGSTGG 345

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RESULT 2
US-09-457-066-2
; Sequence 2, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match          99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 4.8e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 61 PREPHTYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTTIL 120
QY 121 GRMGSGTVPGKQISKGNQIRIFVSDYFPPSPGFCIHNIYMPQTEAVSPSVLPSPA 180
DB 121 GRMGSGTVPGKQISKGNQIRIFVSDYFPPSPGFCIHNIYMPQTEAVSPSVLPSPA 180
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DB 241 LEEVRLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGACCLHNCNECQVPSK 300
QY 301 VTKKYEVLQLRPKTGVRLGKSLTDVLEHHECCDVCVCGSTGG 345
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RESULT 3
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; Sequence 2, Application US/09265686
; Patent No. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: P1122P2
; CURRENT APPLICATION NUMBER: US/09/265,686
; CURRENT FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
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Best Local Similarity 99.4%; Pred. No. 4.8e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 61 PREPHTYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTTIL 120
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DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVGRKSRVVDNL 240
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DB 241 LEEVRLYSCTPRNFSVSIREEELKRTDTIFWPGCLLVKRCGACCLHNCNECQVPSK 300
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US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-5

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Best Local Similarity 99.4%; Pred. No. 4.8e-193;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 61 PREPHTYPRNTVLVWRLVAEENWVQLTFDERFGLEDPEDDICKYDFVEEPPSDGTTIL 120
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Qy      119 --ILGRWCGSGTVPKQKISKNOIRIRFVSDPEFPGFCIHYNIMPOFTAV----- 171
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Qy      172 -----SPSVLPSPALPLDLNNAITASTLEDLIRYLEPERWOLDEDLYR 217
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; Sequence 4, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; EARLIER FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-540-224-4

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Best Local Similarity 44.0%; Pred. No. 8.4e-72;
Matches 153; Conservative 59; Mismatches 103; Indels 33; Gaps 9;

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Qy      295 QCVPSYTKKHYEVLQLRP---KTGYRGLHKSLLTDALHEHHEECDCVC 339
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RESULT 9
US-08-872-757-2
; Sequence 2, Application US/08872757
; Patent No. 6258564
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Alexander
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,757
; FILING DATE: 10-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,187
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-028-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNITE
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-757-2

Query Match          9.3%; Score 172.5; DB 4; Length 730;
Best Local Similarity 36.6%; Pred. No. 7.3e-10;
Matches 49; Conservative 20; Mismatches 48; Indels 17; Gaps 7;

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; Patent No. 5807981
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Stieron, Aleksander
; APPLICANT: Brenner, Mitch
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
; TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,225
; FILING DATE: 13-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluid, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-572-225-1

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Best Local Similarity 39.4%; Pred. No. 2e-09;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

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OY 114 --PSDGTILGRMGSGTVPGKQISKGNOIRIRFVSDEYFPSEPGFCHY 160
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Db 456 GLTADSKLHGKFCGS-EKPEVITSQYNMNRKESDNTV-SKKGFAHF 502

RESULT 11
US-08-936-135-18
; Sequence 18, Application US/08936135
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: He, Zhigang
; APPLICANT: Chen, Hang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 909 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-936-135-18

Query Match          8.9%; Score 164.5; DB 3; Length 909;
Best Local Similarity 29.9%; Pred. No. 7.5e-09;
Matches 49; Conservative 20; Mismatches 70; Indels 25; Gaps 5;

OY 1 MSLFGLLVTSALAGRRGTQAESNLSSKPFSSNKQNGVQDPQHERLITVSTNGSIHS 60
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1 MDMEPLTWVFLA-----YSRHQVRGQPPPCGGRLNSKDAQYIIS 42

OY 61 PRPHPTYPRTVTVLWRLVAEENWVQLTFDERFGLEDEDDICKYDFVEVE--EPSDGT 118
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 43 PGYPDYPSSHQNCWEIVYAPPEPNQKIVLNFNPHFEIEKHD---CKYDFLEIRGDSESD 99

OY 119 ILGRMGSGTVPGKQISKGNOIRIRFVSDEYFPSEPGFCHYNI 162
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 100 LLSKMGCN-IAPPTIISGSMLYIKFTSD-YANQAGAFSLUREI 141

RESULT 12
US-08-936-135-20
; Sequence 20, Application US/08936135
; Patent No. 6054293
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: He, Zhigang
; APPLICANT: Chen, Hang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/116,473
FILING DATE: 17-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/052,762
FILING DATE: 17-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.74973
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-116-473-2

Query Match 8.8%; Score 163; DB 4; Length 925;
Best Local Similarity 33.8%; Pred. No. 1.1e-08;
Matches 45; Conservative 20; Mismatches 60; Indels 8; Gaps 5;
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DB 15 FSGHKVRS-QQDPCCGRKNSKDAGYITSPGYQDIPSHONCEWVYAPENOKIVLNFN 73
QY 92 ERGLDEPDDEDDICKYDVEVE--EPSDGTILGRWCGSGTVPGKQISKGNQIRIFVSDEY 149
DB 74 PHEIEIKHD--CKYDFEIRDDSDSADLLGRHCGN-IPFTIISGSVLYIKFTSD-Y 128
QY 150 FSESPGFCIHNT 162
DB 129 AROGAGFSLRYEI 141

Search completed: April 29, 2003, 09:09:16
Job time : 15.5 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 08:57:36 ; Search time 33.5 Seconds
(without alignments)
1372.283 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858
Sequence: 1 MSFLGLLVTSALAGGRCT.....DYALEHNEEDCVCRGSTG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :
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23: /SID52/gcgdata/geneseq/genesqp-emb1/AA2002.DAT:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	100.0	345	21	AAV84557
2	1858	100.0	345	23	AAE13212
3	1851	99.6	345	20	AAV33579
4	1851	99.6	345	20	AAV41766
5	1851	99.6	345	20	AAV30023
6	1851	99.6	345	21	AAAB8657
7	1851	99.6	345	21	AAAB24250
8	1851	99.6	345	21	AAAB4322
9	1851	99.6	345	21	AAAB10533
10	1851	99.6	345	21	AAAB10635

11	1851	99.6	345	21	AAAB10644	Human VEGF-X prote
12	1851	99.6	345	21	AAAB10650	Human 990126vegX p
13	1851	99.6	345	21	AAAB10651	Human VEGF-X prote
14	1851	99.6	345	21	AAAB19578	Human PRO200 (vasc
15	1851	99.6	345	21	AAAB33414	Human PRO200 prote
16	1851	99.6	345	21	AAAB24412	Human PRO713 prote
17	1851	99.6	345	21	AAAB01419	Human TANGO 128.
18	1851	99.6	345	21	AAV96858	Human growth facto
19	1851	99.6	345	21	AAV59285	Bone morphogenic p
20	1851	99.6	345	22	AAV65603	Human zveg13 polyp
21	1851	99.6	345	22	AAU08465	Polyptide for hu
22	1851	99.6	345	22	AAU12314	Human PRO200 polyp
23	1851	99.6	345	22	AAV74028	Human VEGF/PDGF-11
24	1851	99.6	345	22	AAE02649	Human LP8, a PDGF-
25	1851	99.6	345	22	AAE00997	Human zveg13 prote
26	1851	99.6	345	22	AAV50980	Human PRO200 prote
27	1851	99.6	345	22	AAV49895	Human PRO200 prote
28	1851	99.6	345	22	AAV53074	Human angiogenesis
29	1851	99.6	345	23	AAV81331	Human VEGF/PDGF-11
30	1851	99.6	345	23	AAV47889	Human zveg13. Hom
31	1851	99.6	345	23	AAV76684	Human zveg13 prote
32	1851	99.6	345	21	AAAB10639	Human VEGF-X prote
33	1843	99.2	345	21	AAAB10634	Human VEGF-X homol
34	1843	99.2	345	21	AAAB10636	Human VEGF-X prote
35	1843	99.2	345	21	AAAB03003	Human growth facto
36	1745	93.9	354	21	AAAB10640	Human VEGF-X prote
37	1745	93.9	354	21	AAAB10641	Human VEGF-X prote
38	1728	93.0	318	21	AAV84558	A fragment of plat
39	1674.5	90.1	339	21	AAV58438	Lung cancer associ
40	1664	89.6	345	21	AAV48658	Mouse zveg13, SEQ
41	1664	89.6	345	21	AAV96861	Murine vascular en
42	1664	89.6	345	21	AAV84559	Mouse platelet-
43	1664	89.6	345	22	AAE00998	Mouse zveg13 prote
44	1664	89.6	345	23	AAV7890	Mouse zveg13. Mus
45	1664	89.6	345	23	AAE13213	Mouse platelet-der

ALIGNMENTS

RESULT 1
AAV84557
ID AAV84557 standard; Protein: 345 AA.
XX
AC AAV84557;
XX
DT 25-JUL-2000 (first entry)
XX
XX Amino acid sequence of platelet-derived growth factor C (PDGF-C).
DE Platelet-derived growth factor C: PDGF-C; cell proliferation;
XX fibroblast mitogenesis; wound healing; VEGF-F;
XX growth factor; heparin; connective tissue; tumour growth;
KW Choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
KW Lung carcinoma; erythroleukemia; tissue remodelling.
XX
XX Homo sapiens.
OS
PN WO200018212-A2.
XX
PD 06-APR-2000.
XX
PF 30-SEP-1999; 99WO-US22668.
XX
XX 30-SEP-1998; 98US-0102461.
PR 12-NOV-1998; 98US-0108109.
PR 03-DEC-1998; 98US-0110749.
PR 18-DEC-1998; 98US-0113002.
PR 21-MAY-1999; 99US-0135426.
PR 15-JUL-1999; 99US-0144022.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD.

XX Eriksson U, Aase K, Lee X, Ponten A, Uutela M, Alitalo K;
PI Oestman A, Heldin C, Betsholtz C;
XX
XX WPI: 2000-292954/25.
DR N-PSDB: AAA12523.
XX
XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
PT differentiation, growth and motility of cells expressing the PDGF-C
PT receptor
XX
XX Claim 27: Fig 2: 135pp: English.
XX
XX The present sequence represents human platelet-derived growth factor C
CC (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the
CC ability to stimulate and enhance proliferation or differentiation,
CC and/or growth or motility of cells expressing a PDGF-C receptor.
CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
CC proliferation, preferably in combination with one other growth factor
CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
CC be used for stimulating connective tissue or wound healing. The
CC PDGF-C polypeptide can be enzymatically processed to generate the active
CC truncated form of PDGF-C and used to regulate the receptor-binding
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
CC and erythroleukemia, can be identified by testing for expression of
CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
CC remodelling during invasion of tumour cells into a normal population of
CC cells. Antagonists can also be used to treat fibrotic conditions,
CC especially found in the lung, kidney or liver.
XX
XX Sequence 345 AA:
SO
Query Match 100.0%; Score 1858; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.7e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLEGLLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHRRITTVSTNGSIHS 60
Db 1 MSLEGLLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHRRITTVSTNGSIHS 60
QY 61 PRPHHTYPRNTVLVWRLVAVEENWVQLTFDERGLEDPEDDICKYDFVEVEERSDGTIL 120
Db 61 PRPHHTYPRNTVLVWRLVAVEENWVQLTFDERGLEDPEDDICKYDFVEVEERSDGTIL 120
QY 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEFGFCIHNIYVPOFTEAVSPSLPPSA 180
Db 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEFGFCIHNIYVPOFTEAVSPSLPPSA 180
QY 181 LPDLNNAATTAFTSTEDLRLYLEPERWQDLDELYRPTMQLGKAFVFGKSRVVDNL 240
Db 181 LPDLNNAATTAFTSTEDLRLYLEPERWQDLDELYRPTMQLGKAFVFGKSRVVDNL 240
QY 241 LEEVRLYSTCPRNFSYSIREELKRTDTIFWPGCLLVKRCGACACACAHNCNEOCVPSK 300
Db 241 LEEVRLYSTCPRNFSYSIREELKRTDTIFWPGCLLVKRCGACACACAHNCNEOCVPSK 300
QY 301 VTKKYHEVLDLRPKTYGRLGKSLTDVLEHNEBCDCVCGSTGG 345
Db 301 VTKKYHEVLDLRPKTYGRLGKSLTDVLEHNEBCDCVCGSTGG 345
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AAE13212
ID AAE13212 standard; Protein: 345 AA.
XX
XX AAE13212:
XX
XX 12-FEB-2002 (first entry)
XX

DE Human platelet-derived growth factor (PDGF-C) protein.
XX
XX Human: transgenic animal; platelet derived growth factor C; PDGF-C;
KW cardiac hypertrophy; fibrosis.
XX
XX Homo sapiens.
OS
PN WO200172132-A1.
XX
XX 04-OCT-2001.
PD
XX 28-MAR-2001; 2001WO-US09855.
PE
XX 28-MAR-2000; 2000US-192507P.
PR
XX (LUDM-) LUDWIG INST CANCER RES.
PA
XX Eriksson U, Li X, Ponten A, Aase K, Li H;
PI WPI: 2002-010700/01.
DR
XX A transgenic animal over-expressing platelet derived growth factor C is
PT useful to study and find therapy for disease associated with PDGF-C
PT over-expression, including cardiac hypertrophy and fibrosis
XX
XX Disclosure: Page 40-42; 48pp: English.
XX
XX The patent discloses a method for producing a transgenic, non-human
CC animal over-expressing a platelet derived growth factor C (PDGF-C),
CC or its functional fragment or analogue. The method involves introducing
CC a transgenic PDGF-C DNA into a cell of a non-human animal, introducing
CC the cell into a non-human animal and allowing the cell to develop into
CC a transgenic, non-human animal. The transgenic animal is useful as a
CC model to study disease states characterised by over-expression of PDGF-C
CC and to find therapy for those diseases, particularly hypertrophy and
CC fibrosis in various organs including the heart. The present sequence
CC is PDGF-C protein from human.
XX
XX Sequence 345 AA:
SO
Query Match 100.0%; Score 1858; DB 23; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.7e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLEGLLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHRRITTVSTNGSIHS 60
Db 1 MSLEGLLLVTSALAGRGTOAESNLSSKFOFSSNKEONGVODPOHRRITTVSTNGSIHS 60
QY 61 PRPHHTYPRNTVLVWRLVAVEENWVQLTFDERGLEDPEDDICKYDFVEVEERSDGTIL 120
Db 61 PRPHHTYPRNTVLVWRLVAVEENWVQLTFDERGLEDPEDDICKYDFVEVEERSDGTIL 120
QY 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEFGFCIHNIYVPOFTEAVSPSLPPSA 180
Db 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPPSEFGFCIHNIYVPOFTEAVSPSLPPSA 180
QY 181 LPDLNNAATTAFTSTEDLRLYLEPERWQDLDELYRPTMQLGKAFVFGKSRVVDNL 240
Db 181 LPDLNNAATTAFTSTEDLRLYLEPERWQDLDELYRPTMQLGKAFVFGKSRVVDNL 240
QY 241 LEEVRLYSTCPRNFSYSIREELKRTDTIFWPGCLLVKRCGACACACAHNCNEOCVPSK 300
Db 241 LEEVRLYSTCPRNFSYSIREELKRTDTIFWPGCLLVKRCGACACACAHNCNEOCVPSK 300
QY 301 VTKKYHEVLDLRPKTYGRLGKSLTDVLEHNEBCDCVCGSTGG 345
Db 301 VTKKYHEVLDLRPKTYGRLGKSLTDVLEHNEBCDCVCGSTGG 345
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AAI33679
ID AAI33679 standard; Protein: 345 AA.
XX

[illegible]

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Oy	121	GRMGSGTVPGKQJISKGNQIRFVSDSEYFPESEGFCEIHNIYMPQFTEAVSPVLPISA	180
Db	121	GRMGSGTVPGKQJISKGNQIRFVSDSEYFPESEGFCEIHNIYMPQFTEAVSPVLPISA	180
Oy	181	LPDOLLNNAITAFSTLEDLIRYLERPEWOLDLEDLYRPTMQLLKGAFVGRKSRVVDNL	240
Db	181	LPDOLLNNAITAFSTLEDLIRYLERPEWOLDLEDLYRPTMQLLKGAFVGRKSRVVDNL	240
Oy	241	LTEEVRITSCYPRNFVSYSIREELKRTPTIIFWPGCLVYKRCGNCACCLHNHCNECQVPSK	300
Db	241	LTEEVRITSCYPRNFVSYSIREELKRTPTIIFWPGCLVYKRCGNCACCLHNHCNECQVPSK	300
Oy	301	VTKKYHEVLDLRPKTVGRGLKSLTDVALHNHEECDCVCGSGTGG	345
Db	301	VTKKYHEVLDLRPKTVGRGLKSLTDVALHNHEECDCVCGSGTGG	345

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XX	AA41766 standard; Protein; 345 AA.
XX	AA41766;
XX	07-DEC-1999 (first entry)
XX	Human PRO200 protein sequence.
XX	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW	secreted protein; transmembrane protein.
XX	
OS	Homo sapiens.
XX	
PN	W09946281-A2.
XX	
PD	16-SEP-1999.
XX	
PF	08-MAR-1999; 99WO-US05028.
XX	
PR	10-MAR-1998; 98US-0077450.
PR	11-MAR-1998; 98US-0077632.
PR	11-MAR-1998; 98US-0077641.
PR	11-MAR-1998; 98US-0077649.
PR	12-MAR-1998; 98US-0077791.
PR	13-MAR-1998; 98US-0078004.
PR	17-MAR-1998; 98US-0040220.
PR	20-MAR-1998; 98US-0078886.
PR	20-MAR-1998; 98US-0078910.
PR	20-MAR-1998; 98US-0078936.
PR	20-MAR-1998; 98US-0078939.
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PR	27-MAR-1998; 98US-0079785.
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PR	30-MAR-1998; 98US-0079923.
PR	31-MAR-1998; 98US-0080105.
PR	31-MAR-1998; 98US-0080107.
PR	31-MAR-1998; 98US-0080165.
PR	31-MAR-1998; 98US-0080327.
PR	01-APR-1998; 98US-0080327.
PR	01-APR-1998; 98US-0080328.
PR	01-APR-1998; 98US-0080333.
PR	01-APR-1998; 98US-0080334.
PR	08-APR-1998; 98US-0081049.
PR	08-APR-1998; 98US-0081070.

PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX (GETH) GENENTECH INC.
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
PI
XX WPI; 1999-551358/46.
DR N-PSDB; AA234296.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX
XX Claim 12; Fig 207; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
CC

CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA23891 to
CC AA23438, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
XX Sequence 345 AA:
SQ
Query Match 99.6%; Score 1851; DB 20; Length 345;
Best Local Similarity 99.4%; Pred. No. 8, 9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLEGLLLVTSALAGQRRGTOAESNLSSKFOFSSNKDQNGVDPQHRITVSTNGSIHS 60.
DB 1 MSLEGLLLVTSALAGQRRGTOAESNLSSKFOFSSNKDQNGVDPQHRITVSTNGSIHS 60
QY 61 PRPHYTPRNTVLWRLVAVEENWITQTDPERGLDDEPDICKYPVEEPESDCTIL 120
DB 61 PRPHYTPRNTVLWRLVAVEENWITQTDPERGLDDEPDICKYPVEEPESDCTIL 120
QY 121 GRMGSGTVPGKOISKQNOIRIRFVSDEFPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180
DB 121 GRMGSGTVPGKOISKQNOIRIRFVSDEFPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180
QY 181 LPDLDLNNAITASTLEDLIRYLEPERWOLDLEDLYPPTMQLGKAFVGRKSRVVDLNL 240
DB 181 LPDLDLNNAITASTLEDLIRYLEPERWOLDLEDLYPPTMQLGKAFVGRKSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIPEELKRTDTIFMPGCLLYKRGSGNACCLHNCNCCVPSK 300
DB 241 LTEEVRLYSCTPRNFSVSIPEELKRTDTIFMPGCLLYKRGSGNACCLHNCNCCVPSK 300
QY 301 VTKKYHEVLQLRPTGYRGGLHKSITDVALHNEHCDCVCGSGTGG 345
DB 301 VTKKYHEVLQLRPTGYRGGLHKSITDVALHNEHCDCVCGSGTGG 345
RESULT 5
AA30023
ID AA30023 standard; Protein; 345 AA.
XX
XX AA30023:
AC
XX 11-OCT-1999 (first entry)
DT
XX
DE Human vascular endothelial growth factor related protein.
XX
XX Vascular endothelial growth factor related protein; VEGF-R protein;
KW tissue growth inhibition; tumour growth; cancer; tissue growth;
KW angiogenesis; coronary artery blockage.
XX
XX Homo sapiens.
OS
XX
XX WO9937671-A1.
PN
XX 29-JUL-1999.
PD
XX
XX 26-JAN-1999; 99WO-US01574.
PF
XX
XX 31-AUG-1998; 98US-0098548.
PR 27-JAN-1998; 98US-0072635.
PR 05-JUN-1998; 98US-0080809.
PR 24-JUN-1998; 98US-0090544.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Dou S, Na S, Song HY;
PI
XX

DR MPI: 1999-458680/38.
DR N-PSDB: AAX86352.
XX A vascular endothelial growth factor related protein and related
PT polynucleotide, useful for identifying antagonists and binding
PT compounds
XX
XX
PS Claim 1; Page 56-58; 62pp; English.
XX
XX The present sequence represents a vascular endothelial growth factor
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
CC compounds that bind to it or that antagonize its activity. VEGF-R
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
CC tissue growth. This is useful for inhibiting tumour growth and for
CC treating cancer. VEGF-R itself can be used to stimulate tissue
CC growth, angiogenesis and to treat coronary artery blockage. The
CC VEGF-R coding sequence can be used for the recombinant production of
CC the VEGF-R protein.
XX
XX
SQ Sequence 345 AA:
Query Match 99.6%; Score 1851; DB 20; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSFLGILLVTSALAGRGTOAESNLSSKFOFSSNKEONGVOPQHERITVTGNSIHS 60
DB 1 MSFLGILLVTSALAGRGTOAESNLSSKFOFSSNKEONGVOPQHERITVTGNSIHS 60
OY 61 PREPHYPRNTVLVWRLVAEENVMWQLTFDERFGLEDPEDDICKYDFVEEESPDTIL 120
DB 61 PREPHYPRNTVLVWRLVAEENVMWQLTFDERFGLEDPEDDICKYDFVEEESPDTIL 120
OY 121 GRWCGSTVPGKQISGNQIRIFVSDYRPSRPGCIHNINYPQTEAVSSVLPSPA 180
DB 121 GRWCGSTVPGKQISGNQIRIFVSDYRPSRPGCIHNINYPQTEAVSSVLPSPA 180
OY 181 LPLDLNNATTAFTSTLEDLRIYLEPERWQDLEDLYRPTQGLGKAFVFRKSRVVDNL 240
DB 181 LPLDLNNATTAFTSTLEDLRIYLEPERWQDLEDLYRPTQGLGKAFVFRKSRVVDNL 240
OY 241 LEEVRLYSCPTPNFSVSIREEELKRTDTIFWPGCLLVKRCGACCLHNCNCCVPSK 300
DB 241 LEEVRLYSCPTPNFSVSIREEELKRTDTIFWPGCLLVKRCGACCLHNCNCCVPSK 300
OY 301 VTKKYHEVLIOLRPKTGVRGLHKSITDVALEHHECCDCVCRGSTGG 345
DB 301 VTKKYHEVLIOLRPKTGVRGLHKSITDVALEHHECCDCVCRGSTGG 345
RESULT 6
AAB48657
ID AAB48657 standard; Protein: 345 AA.
XX
XX AAB48657;
XX
DT 09-MAR-2001 (first entry)
XX
XX Human zvegfg3, SEQ ID NO:33.
XX
XX Human; zvegfg3; zvegfg4 fusion; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnerrary; ischaemia;
KW immunomodulation; hepatic.
XX
XX Homo sapiens.
XX
XX MO2000066736-A1.
XX
XX 09-NOV-2000.
XX

PF 03-MAY-2000; 2000MO-US40047.
XX
XX 03-MAY-1999; 99US-0304216.
PR 10-NOV-1999; 99US-0164463.
PR 04-FEB-2000; 2000US-0180169.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX
PI Gilbert T, Hart CE, Shepard PO, Gilbertson DG;
XX
XX MPI: 2000-687541/67.
DR N-PSDB: AAC81582.
XX
XX
PT growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease -
XX
XX
PS Claim 48; Page 125-126; 143pp; English.
XX
XX
XX The invention relates to the human growth factor homologue zvegfg4
CC (AAB48653) and nucleic acids encoding it (AAC81555). zvegfg4 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. zvegfg4 has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. zvegfg4 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3
CC fusions; expression constructs and host cells comprising human zvegfg4
CC nucleic acids; the recombinant expression of human zvegfg4; an antibody
CC which binds to human zvegfg4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zvegfg4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zvegfg4 gene of a patient. zvegfg4 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells, which may be useful in the
CC treatment of ischemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents human zvegfg3.
XX
XX
SQ Sequence 345 AA:
Query Match 99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSFLGILLVTSALAGRGTOAESNLSSKFOFSSNKEONGVOPQHERITVTGNSIHS 60
DB 1 MSFLGILLVTSALAGRGTOAESNLSSKFOFSSNKEONGVOPQHERITVTGNSIHS 60
OY 61 PREPHYPRNTVLVWRLVAEENVMWQLTFDERFGLEDPEDDICKYDFVEEESPDTIL 120
DB 61 PREPHYPRNTVLVWRLVAEENVMWQLTFDERFGLEDPEDDICKYDFVEEESPDTIL 120
OY 121 GRWCGSTVPGKQISGNQIRIFVSDYRPSRPGCIHNINYPQTEAVSSVLPSPA 180
DB 121 GRWCGSTVPGKQISGNQIRIFVSDYRPSRPGCIHNINYPQTEAVSSVLPSPA 180
OY 181 LPLDLNNATTAFTSTLEDLRIYLEPERWQDLEDLYRPTQGLGKAFVFRKSRVVDNL 240
DB 181 LPLDLNNATTAFTSTLEDLRIYLEPERWQDLEDLYRPTQGLGKAFVFRKSRVVDNL 240
OY 241 LEEVRLYSCPTPNFSVSIREEELKRTDTIFWPGCLLVKRCGACCLHNCNCCVPSK 300
DB 241 LEEVRLYSCPTPNFSVSIREEELKRTDTIFWPGCLLVKRCGACCLHNCNCCVPSK 300

QY 301 VTKKYEVLQLRPKTGVRLHKSITDVALHNEHCDCVCGSTGG 345
 |||||
 Db 301 VTKKYEVLQLRPKTGVRLHKSITDVALHNEHCDCVCGSTGG 345

RESULT 7
 AAB24250
 ID AAB24250 standard; Protein; 345 AA.
 XX
 AC AAB24250;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human platelet-derived growth factor related protein LP8.
 XX
 DE Human; platelet derived growth factor related protein; LP8. VEGFh.
 KW vascular endothelial growth factor h; tissue regeneration; vulinerary;
 KW atherosclerosis; PDGF-related protein; antiarteriosclerotic.
 XX
 OS Homo sapiens.
 OS
 PN MO200059940-A2.
 PD 12-OCT-2000.
 XX
 PF 24-MAR-2000; 2000MO-US06427.
 XX
 PR 06-APR-1999; 99US-0127913.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Hammond LJ, Na S;
 XX
 DR MPI: 2000-664991/64.
 DR N-PSDB; AAC64426.
 XX
 PT Enhancing tissue growth and promoting wound healing by administering
 PT platelet-derived growth factor related protein, LP8 or its analog and
 XX treating atherosclerosis by administering LP8 antagonist
 XX
 PS Claim 4; Page 63-64; 64pp; English.
 XX
 CC The present invention describes a method for enhancing tissue growth,
 CC promoting wound healing or stimulating smooth muscle growth by
 CC administering a platelet-derived growth factor (PDGF) related protein,
 CC designated LP8 or its analogue. Also described is a method of slowing
 CC the progress of atherosclerosis or treating atherosclerosis comprising
 CC the administration of an LP8 antagonist. The method is useful for
 CC enhancing tissue growth, promoting wound healing and stimulating smooth
 CC muscle growth. Antagonists of LP8 are useful for treating
 CC atherosclerosis. The present sequence represents human LP8, which is
 CC also called VEGFh.
 XX
 SQ Sequence 345 AA;
 XX

Query Match 99.6%; Score 1851; DB 21; Length 345;
 Best Local Similarity 99.4%; Pred. No. 8, 9e-179;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLVTALAGRRGTQAESNLSSKRFQSSNKRQNGVODPQHERITVSTNGSIHS 60
 |||||
 Db 1 MSLEGLLVTALAGRRGTQAESNLSSKRFQSSNKRQNGVODPQHERITVSTNGSIHS 60

QY 61 PREPHRYPRNTVLMVRLVAVENWMIQITDERGLEDPEDDICKYDFVEEESDGTIL 120
 |||||
 Db 61 PREPHRYPRNTVLMVRLVAVENWMIQITDERGLEDPEDDICKYDFVEEESDGTIL 120

QY 121 GRMGSGTGVGKQISKQNOIRIRFVSDPEPSPFCIHYNIVMPOTFEAVSPVLPSSA 180
 |||||
 Db 121 GRMGSGTGVGKQISKQNOIRIRFVSDPEPSPFCIHYNIVMPOTFEAVSPVLPSSA 180

QY 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLLEDLYRPTQQLGKAFVFGRRSRVVDLNL 240

Db 181 LPDLNNATTAFTSTLEDLIRYLEPERWQDLLEDLYRPTQQLGKAFVFGRRSRVVDLNL 240
 |||||
 QY 241 LTFEVRLYSCTPRNFESVSTIEELKRTDTIFWPGCLLVKRCGACCLHNCNCOCVPSK 300
 |||||
 Db 241 LTFEVRLYSCTPRNFESVSTIEELKRTDTIFWPGCLLVKRCGACCLHNCNCOCVPSK 300

QY 301 VTKKYEVLQLRPKTGVRLHKSITDVALHNEHCDCVCGSTGG 345
 |||||
 Db 301 VTKKYEVLQLRPKTGVRLHKSITDVALHNEHCDCVCGSTGG 345

RESULT 8
 AAB44322
 ID AAB44322 standard; Protein; 345 AA.
 XX
 AC AAB44322;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
 XX
 DE Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 KW expressed sequence tag; detection; cancer.
 XX
 OS Homo sapiens.
 OS
 PN MO200053756-A2.
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000MO-US04341.
 XX
 PR 08-MAR-1999; 99MO-US05028.
 PR 12-MAR-1999; 99US-0123857.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99MO-US28313.
 PR 02-DEC-1999; 99MO-US28551.
 PR 16-DEC-1999; 99MO-US30095.
 PR 30-DEC-1999; 99MO-US31243.
 PR 30-DEC-1999; 99MO-US31274.
 PR 05-JAN-2000; 2000MO-US00219.
 PR 06-JAN-2000; 2000MO-US00277.
 PR 06-JAN-2000; 2000MO-US00376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Petrarra N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kijavrin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 DR MPI: 2000-611443/58.
 DR N-PSDB; AAC78582.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities.
 XX
 PS Claim 12; Fig 207; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting

CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.

XX Sequence 345 AA:

Query Match 99.6%; Score 1851; DB 21; Length 345;
 Best Local Similarity 99.4%; Pred. No. 8.9e-179;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSLAGRGRTQAESNLSKFOSSNKEONGVODPOHERITTVSTNGSHS 60
 DB 1 MSIFGLLVTSLAGRGRTQAESNLSKFOSSNKEONGVODPOHERITTVSTNGSHS 60
 QY 61 PREPHYPRNTLVMLVAEENVMWQLTFDERFGLEDEPDICKYDFVEEPPSDGTL 120
 DB 61 PREPHYPRNTLVMLVAEENVMWQLTFDERFGLEDEPDICKYDFVEEPPSDGTL 120
 QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEXFPSEPGFCIHYNIMVPOFTAVSPSVLP 180
 DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEXFPSEPGFCIHYNIMVPOFTAVSPSVLP 180
 QY 181 LPDLNLNNAITFASTLEDILRYLEPERWQDLEDILRPTWOLLGKAFVGRKSRVVDNL 240
 DB 181 LPDLNLNNAITFASTLEDILRYLEPERWQDLEDILRPTWOLLGKAFVGRKSRVVDNL 240
 QY 241 LTFEENVLVSCTPRNFSVSIREELKRTDTTFMPGCLLYKRCGNCACCLNNECCVPSK 300
 DB 241 LTFEENVLVSCTPRNFSVSIREELKRTDTTFMPGCLLYKRCGNCACCLNNECCVPSK 300
 QY 301 VTKKYEVLQLRPKTGVRGLHKSITDVALEHHECCDVCGRSGTG 345
 DB 301 VTKKYEVLQLRPKTGVRGLHKSITDVALEHHECCDVCGRSGTG 345

RESULT 9

ID AAB10633 standard; Protein: 345 AA.

XX AAB10633;

DT 19-JAN-2001 (first entry)

XX Human RACE generated VEGF-X protein.

XX VEGF-X: vascular endothelial growth factor; human; vulnery; cytostatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99MO-US30503.

XX 22-DEC-1998; 98GB-0028377.

XX 18-MAR-1999; 99US-0124967.

XX 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;
 PI Dhanraj SM, Xu J;

DR WPI: 2000-442669/38.
 DR N-PSDB: AAA71951.

PT New vascular endothelial growth factor protein, useful for treating or
 PT preventing diseases associated with inappropriate angiogenesis activity
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure: Fig 6: 127pp: English.

CC This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
 CC vulnery, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
 CC antidiabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation of tissues, tissue regeneration and organ
 CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents the RACE generated human VEGF-X
 CC protein described in the method of the invention.

XX Sequence 345 AA:

Query Match 99.6%; Score 1851; DB 21; Length 345;
 Best Local Similarity 99.4%; Pred. No. 8.9e-179;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSLAGRGRTQAESNLSKFOSSNKEONGVODPOHERITTVSTNGSHS 60
 DB 1 MSIFGLLVTSLAGRGRTQAESNLSKFOSSNKEONGVODPOHERITTVSTNGSHS 60
 QY 61 PREPHYPRNTLVMLVAEENVMWQLTFDERFGLEDEPDICKYDFVEEPPSDGTL 120
 DB 61 PREPHYPRNTLVMLVAEENVMWQLTFDERFGLEDEPDICKYDFVEEPPSDGTL 120
 QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEXFPSEPGFCIHYNIMVPOFTAVSPSVLP 180
 DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEXFPSEPGFCIHYNIMVPOFTAVSPSVLP 180
 QY 181 LPDLNLNNAITFASTLEDILRYLEPERWQDLEDILRPTWOLLGKAFVGRKSRVVDNL 240
 DB 181 LPDLNLNNAITFASTLEDILRYLEPERWQDLEDILRPTWOLLGKAFVGRKSRVVDNL 240
 QY 241 LTFEENVLVSCTPRNFSVSIREELKRTDTTFMPGCLLYKRCGNCACCLNNECCVPSK 300
 DB 241 LTFEENVLVSCTPRNFSVSIREELKRTDTTFMPGCLLYKRCGNCACCLNNECCVPSK 300
 QY 301 VTKKYEVLQLRPKTGVRGLHKSITDVALEHHECCDVCGRSGTG 345
 DB 301 VTKKYEVLQLRPKTGVRGLHKSITDVALEHHECCDVCGRSGTG 345

RESULT 10

ID AAB10635 standard; Protein: 345 AA.

XX AAB10635;

DT 19-JAN-2001 (first entry)

XX Human VEGF-X protein #1 isolated from clones 4 and 7.

XX VEGF-X: vascular endothelial growth factor; human; vulnery; cytostatic;
 KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.

```

XX OS Homo sapiens.
XX PN WO200037641-A2.
XX PD 29-JUN-2000.
XX PF 21-DEC-1999; 99WO-US30503.
XX PR 22-DEC-1998; 98GB-0028377.
XX PR 18-MAR-1999; 99US-0124967.
XX PR 08-NOV-1999; 99US-0164131.
XX PA (JANC ) JANSSEN PHARM NV.
XX PI Gordon RD, Sprengel JJ, Von JR, Dijkmans JHH, Goslowska A;
XX PI Dhanaraj SN, Xu J;
XX DR WPI: 2000-442669/38.
XX DR N-PSDB: AAA71955.
XX PT New vascular endothelial growth factor protein, useful for treating or
XX PT preventing diseases associated with inappropriate angiogenesis activity
XX PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX PS Disclosure; Fig 9, 127pp; English.
XX CC This invention describes a novel vascular endothelial growth factor-X
XX CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
XX CC vulnerability, cyclostatic, antirheumatic, antiarthritic, antipsoriatic and
XX CC antidiabetic activity and acts as an angiogenesis and vascularization
XX CC regulator. An antisense molecule of the invention is useful for treating
XX CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX CC retinopathy by inhibiting angiogenic activity or inappropriate
XX CC vascularization including formation and proliferation of new blood
XX CC vessels, growth and development of tissues, tissue regeneration and organ
XX CC and tissue repair in a subject. The products of the invention are useful
XX CC for preparing medicaments for treating wounds such as dermal ulcers,
XX CC pressure sores, venous sores, diabetic ulcers and burns and to promote
XX CC skin graft growth, tissue repair, proliferation of new blood vessels,
XX CC tissue regeneration and organ repair by promoting angiogenic activity or
XX CC vascularization. This sequence represents the human VEGF-X protein
XX CC isolated from clones 4 and 7 described in the method of the invention.
XX XX
XX SQ Sequence 345 AA:
XX
XX Query Match 99.6%; Score 1851; DB 21; Length 345;
XX Best Local Similarity 99.4%; Pred. No. 8.9e-179;
XX Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSLEGLLLVTSALAGRGRTQAESNLSSKRFQSSNKEONGVODPOHERITVSTNGSIHS 60
DB 1 MSLEGLLLTSALAGRGRTQAESNLSSKRFQSSNKEONGVODPOHERITVSTNGSIHS 60
OY 61 PREPHYTPNTYLVWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTIL 120
DB 61 PREPHYTPNTYLVWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTIL 120
OY 121 GRMGSGTYPGKQISKGNQIRIRFVSEDEFPSPGFCIHNYIMWPOFTEVSPVLPSSA 180
DB 121 GRMGSGTYPGKQISKGNQIRIRFVSEDEFPSPGFCIHNYIMWPOFTEVSPVLPSSA 180
OY 181 LPDLILNNAITAFSTLEDLIRYLEPERMQLDELDYRPTWQLGKAFVGRKSRVDLNL 240
DB 181 LPDLILNNAITAFSTLEDLIRYLEPERMQLDELDYRPTWQLGKAFVGRKSRVDLNL 240
OY 241 LEEVNLVLCSTPNSVSSTREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCPSPK 300
DB 241 LEEVNLVLCSTPNSVSSTREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCPSPK 300
OY 301 VAKKHEVQLARKRTGVRGLHKSITDYALHHEHCCDCVCRSTNG 345
DB 301 VAKKHEVQLARKRTGVRGLHKSITDYALHHEHCCDCVCRSTNG 345

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RESULT 11
AAB10644
ID AAB10644 standard; Protein; 345 AA.
XX AC AAB10644;
XX DT 19-JAN-2001 (first entry)
XX DE Human VEGF-X protein #4.
XX KW VEGF-X; vascular endothelial growth factor; human; vulnerary; cyclostatic;
XX KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
XX KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
XX KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
XX KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX KW venous sore; diabetic ulcer; burns; skin graft growth.
XX OS Homo sapiens.
XX PN WO200037641-A2.
XX PD 29-JUN-2000.
XX PF 21-DEC-1999; 99WO-US30503.
XX PR 22-DEC-1998; 98GB-0028377.
XX PR 18-MAR-1999; 99US-0124967.
XX PR 08-NOV-1999; 99US-0164131.
XX PA (JANC ) JANSSEN PHARM NV.
XX PI Gordon RD, Sprengel JJ, Von JR, Dijkmans JHH, Goslowska A;
XX PI Dhanaraj SN, Xu J;
XX DR WPI: 2000-442669/38.
XX DR N-PSDB: AAA71950.
XX PT New vascular endothelial growth factor protein, useful for treating or
XX PT preventing diseases associated with inappropriate angiogenesis activity
XX PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX PS Disclosure; Fig 30B; 127pp; English.
XX XX
XX CC This invention describes a novel vascular endothelial growth factor-X
XX CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
XX CC vulnerability, cyclostatic, antirheumatic, antiarthritic, antipsoriatic and
XX CC antidiabetic activity and acts as an angiogenesis and vascularization
XX CC regulator. An antisense molecule of the invention is useful for treating
XX CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX CC retinopathy by inhibiting angiogenic activity or inappropriate
XX CC vascularization including formation and proliferation of new blood
XX CC vessels, growth and development of tissues, tissue regeneration and organ
XX CC and tissue repair in a subject. The products of the invention are useful
XX CC for preparing medicaments for treating wounds such as dermal ulcers,
XX CC pressure sores, venous sores, diabetic ulcers and burns and to promote
XX CC skin graft growth, tissue repair, proliferation of new blood vessels,
XX CC tissue regeneration and organ repair by promoting angiogenic activity or
XX CC vascularization. This sequence represents a human VEGF-X protein
XX CC described in the method of the invention.
XX XX
XX SQ Sequence 345 AA:
XX
XX Query Match 99.6%; Score 1851; DB 21; Length 345;
XX Best Local Similarity 99.4%; Pred. No. 8.9e-179;
XX Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSLEGLLLVTSALAGRGRTQAESNLSSKRFQSSNKEONGVODPOHERITVSTNGSIHS 60
DB 1 MSLEGLLLTSALAGRGRTQAESNLSSKRFQSSNKEONGVODPOHERITVSTNGSIHS 60
OY 61 PREPHYTPNTYLVWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTIL 120

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|||||
Db 61 PRPHPTVPRNTVLVWRLVAVEENWMIQLTFDERFGLDEPEDDICKYDFVEEPPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSPGFCIHNYIMVQPTTEAVSVLPSPA 180
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSPGFCIHNYIMVQPTTEAVSVLPSPA 180
QY 181 LPLDLNNATTAFTSTLEDLIRYLEPERWQDLDELRYPTMQLGKAFVGRKSRVVDNL 240
Db 181 LPLDLNNATTAFTSTLEDLIRYLEPERWQDLDELRYPTMQLGKAFVGRKSRVVDNL 240
QY 241 LTFEVRILYSCTPRNFSYSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCQCVPSPK 300
Db 241 LTFEVRILYSCTPRNFSYSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCQCVPSPK 300
QY 301 VTKKHYEVLQLRPKTGVRGHLKSLTDVALEHHECCVCVCGSTGG 345
Db 301 VTKKHYEVLQLRPKTGVRGHLKSLTDVALEHHECCVCVCGSTGG 345

```

RESULT 12

AAB10650
ID AAB10650 standard; Protein; 345 AA.

AC AAB10650;

DT 19-JAN-2001 (first entry)

DE Human 990126vegx protein.

KW VEGF-X; vascular endothelial growth factor; human; vulnereary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

OS MO200037641-A2.

PN 29-JUN-2000.

PD 21-DEC-1999; 99WO-US30503.

PF 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

PI Gordon RD, Sprengel JJ, Von JR, Dijkmans JH, Goslowska A;

PI Dhanaraj SN, Xu J;

XX MPI; 2000-442669/38;

PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX Disclosure: Fig 11: 127pp: English.

XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,

CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human 990126vegx protein
CC used to illustrate the method of the invention.

SQ Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;

Best Local Similarity 99.4%; Pred. No. 8.9e-179;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSPLGILLVTSALAGRGTOAESNLSSKFOFSSNKEONGVOPQHERITVSTNGSIHS 60
Db 1 MSPLGILLVTSALAGRGTOAESNLSSKFOFSSNKEONGVOPQHERITVSTNGSIHS 60
QY 61 PRPHPTVPRNTVLVWRLVAVEENWMIQLTFDERFGLDEPEDDICKYDFVEEPPSDGTIL 120
Db 61 PRPHPTVPRNTVLVWRLVAVEENWMIQLTFDERFGLDEPEDDICKYDFVEEPPSDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSPGFCIHNYIMVQPTTEAVSVLPSPA 180
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFSPGFCIHNYIMVQPTTEAVSVLPSPA 180
QY 181 LPLDLNNATTAFTSTLEDLIRYLEPERWQDLDELRYPTMQLGKAFVGRKSRVVDNL 240
Db 181 LPLDLNNATTAFTSTLEDLIRYLEPERWQDLDELRYPTMQLGKAFVGRKSRVVDNL 240
QY 241 LTFEVRILYSCTPRNFSYSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCQCVPSPK 300
Db 241 LTFEVRILYSCTPRNFSYSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCQCVPSPK 300
QY 301 VTKKHYEVLQLRPKTGVRGHLKSLTDVALEHHECCVCVCGSTGG 345
Db 301 VTKKHYEVLQLRPKTGVRGHLKSLTDVALEHHECCVCVCGSTGG 345

```

RESULT 13

AAB10651
ID AAB10651 standard; Protein; 345 AA.

AC AAB10651;

DT 19-JAN-2001 (first entry)

DE Human VEGF-X protein #3.

KW VEGF-X; vascular endothelial growth factor; human; vulnereary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

PN MO200037641-A2.

PD 29-JUN-2000.

PF 21-DEC-1999; 99WO-US30503.

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

PI Gordon RD, Sprengel JJ, Von JR, Dijkmans JH, Goslowska A;

PI Dhanaraj SN, Xu J;

XX MPI; 2000-442669/38.

PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX
PS Claim 72: Fig 12; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (1a) and its encoding polynucleotide (1ia) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antiangiogenic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC described in the method of the invention.
XX
XX
SQ Sequence 345 AA:
Query Match 99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSFGLLLVSAAGGRRGTOAESNLSSKFOFSSNKEONGVODPOHERITVSTNGSIHS 60
DB 1 MSFGLLLVSAAGGRRGTOAESNLSSKFOFSSNKEONGVODPOHERITVSTNGSIHS 60
OY 61 PRPHYPRMTVLWRIYAEENWVIOITFERGLEDPEDDICKYFVEEESDSTIL 120
DB 61 PRPHYPRMTVLWRIYAEENWVIOITFERGLEDPEDDICKYFVEEESDSTIL 120
OY 121 GRMGSGTVPKQKSKNOIRIRFVSDPEPSPFCIHYNIVAPQTEAVSPVLPSSA 180
DB 121 GRMGSGTVPKQKSKNOIRIRFVSDPEPSPFCIHYNIVAPQTEAVSPVLPSSA 180
OY 181 LPDLNNAITATSTEDLIRYLEPERWOLDLERYPTWOLGKAFVGRKSVVDLNL 240
DB 181 LPDLNNAITATSTEDLIRYLEPERWOLDLERYPTWOLGKAFVGRKSVVDLNL 240
OY 241 LTFEVRLYSCPRNFVSISIEELKRTDTTFMPGCLLVKRGNCACCLHNCNEQCVPSK 300
DB 241 LTFEVRLYSCPRNFVSISIEELKRTDTTFMPGCLLVKRGNCACCLHNCNEQCVPSK 300
OY 301 VTKKYEVLQLRPKTVGRGLHKSITDVALHNEHCDCVCRGSTG 345
DB 301 VTKKYEVLQLRPKTVGRGLHKSITDVALHNEHCDCVCRGSTG 345
RESULT 14
AAB19578
ID AAB19578 standard; Protein; 345 AA.
XX
XX AAB19578:
AC
XX
XX 22-JAN-2001 (first entry)
DE Human PRO200 (vascular endothelial growth factor E).
XX
XX PRO200: vascular epithelial growth factor E; VEGF-E; human;
KM ocular disease; retinopathy; maculopathy; therapy;
KM retinitis pigmentosa; macular degeneration; retinal detachment;
KM retinal tear; macular hole; myopia; traumatic choroidretinopathy;
KM acute retinal necrosis syndrome; contusion; edema;
KM retinal vision occlusion; vascular disease; retinal vasculitis;
KM thrombocytopenic purpura; uveitis; retinal occlusion.
OS Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..14
FT /label= Signal_Peptide
FT Protein 15..345
FT /label= Mature_Pro200
FT Modified-site 25..29
FT /note= "Asn is N-glycosylated"
FT Modified-site 55..59
FT /note= "Asn is N-glycosylated"
FT Modified-site 254..258
FT /note= "Asn is N-glycosylated"
FT Modified-site 15..21
FT /note= "N-myristoylation"
FT Modified-site 117..123
FT /note= "N-myristoylation"
FT Modified-site 127..133
FT /note= "N-myristoylation"
FT Modified-site 281..287
FT /note= "N-myristoylation"
FT Modified-site 282..288
FT /note= "N-myristoylation"
FT Modified-site 319..325
FT /note= "Amidation"
XX
XX MO200053760-A2.
XX
XX 14-SEP-2000.
XX
XX 10-MAR-2000; 2000WO-US06319.
XX
XX 12-MAR-1999; 99US-0123957.
XX
XX (GETH) GENENTECH INC.
XX
XX Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ, Kabakoff RC;
PI Klein RD, Kljavin J, Kuo SS, La Fleur M, Wood WI;
XX
XX WPI: 2000-587437/55.
XX N-PSDB; AAA88515.
XX
XX Novel PRO polypeptides useful for preventing or rescuing retinal cells
PT from injury caused by ocular diseases such as retinitis pigmentosa,
PT retinopathy, retinal degenerative diseases, degenerative myopia,
PT uveitis -
XX
XX Claim 2: Fig 2; 140pp; English.
XX
XX The present sequence is that of human PRO200 or vascular
CC endothelial growth factor E (VEGF-E), as predicted from a cDNA
CC clone (see AAA88515) that was isolated from a glioma cell line 661
CC library using probes (see AAA88523-26) based on an expressed sequence
CC tag (see AAA88522) that showed homology to VEGF. PRO200 has a
CC predicted mol.wt. of 39,029 and a pI of about 6.06. A method for
CC producing PRO polypeptides, including PRO200, using a host cell
CC transformed with a vector comprising a PRO nucleic acid is claimed.
CC The invention relates to the use of PRO polypeptides to delay,
CC prevent or rescue retinal cells such as retinal neurons selected from
CC photoreceptors, retinal ganglion cells, displaced retinal ganglion
CC cells, amacrine cells, displaced amacrine cells, horizontal and
CC bipolar neurons, and supportive cells (including Muller cells and
CC pigment epithelial cells) from injury and degradation. The retinal
CC cells are preferably photoreceptors and photoreceptor cell injury or
CC death is caused by retinal injury, light or environmental trauma or
CC by an ocular disease selected from retinitis pigmentosa, macular
CC degeneration, including age-related, retinal detachment, retinal
CC tears, retinopathy, retinal degenerative diseases, macular holes,
CC degenerative myopia, acute retinal necrosis syndrome, traumatic
CC choroidretinopathies or contusion such as Purtscher's retinopathy.
CC edema, ischemic conditions such as central or branch retinal vision
CC occlusion, collagen vascular diseases, thrombocytopenic purpura,
CC uveitis, retinal vasculitis and occlusion associated with Fales
CC disease and systemic lupus erythematosus (claimed).

```

XX  Sequence      345 AA:
SQ
Query Match      99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY  1 MSLLGILLVTSALAGRCRQTAESNLKSFQFSNNKQNGVODPOHERITITVSTNGSIHS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  1 MSLLGILLVTSALAGRCRQTAESNLKSFQFSNNKQNGVODPOHERITITVSTNGSIHS 60
OY  61 PPPPHYPRNTVLVWRLVAEENWVLIQLTFDERFGLDEPDICKYDFVEVEEPPSDGTL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  61 PPPPHYPRNTVLVWRLVAEENWVLIQLTFDERFGLDEPDICKYDFVEVEEPPSDGTL 120
OY  121 GWCWGSCTVPGKQISKGNQIRIRFVSDEFESEPGFCIHYNIVMPQETAVSPSVLPSPA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  121 GWCWGSCTVPGKQISKGNQIRIRFVSDEFESEPGFCIHYNIVMPQETAVSPSVLPSPA 180
OY  181 LPDLLNNATFASTLEDLIRYLEPERWQLEDLRYRPTWQLGKAFVGRKSRVVDNL 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  181 LPDLLNNATFASTLEDLIRYLEPERWQLEDLRYRPTWQLGKAFVGRKSRVVDNL 240
OY  241 LTEEVRLISCTPRNFSVSIREELKRTDTITPQCILLVRCGNCACCLHNCNCCQVPSK 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  241 LTEEVRLISCTPRNFSVSIREELKRTDTITPQCILLVRCGNCACCLHNCNCCQVPSK 300
OY  301 VVKKHYEVQLRPKTVGRGLHKSITDVNALEHHHECCDCVCRGSTGG 345
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  301 VVKKHYEVQLRPKTVGRGLHKSITDVNALEHHHECCDCVCRGSTGG 345

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RESULT 15

AAB33414

ID AAB33414 standard: Protein: 345 AA.

AC AAB33414;

DT 29-JAN-2001 (first entry)

DE Human PRO200 protein UNO174 SEQ ID NO:2.

Human; immune related disease; diagnosis; antinflammatory; cardiact;
 dermatological; ankylosing; antineumatic; immunosuppressive;
 haemostatic; antithyroid; antidiabetic; nocrotic; neuroprotective;
 antanaemic; hepatotropic; virucide; antipruritic; antiasthmatic;
 antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
 idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 autoimmune thrombocytopenia; immune-mediated renal disease;
 demyelinating disease; hepatobiliary disease; Whipple's disease;
 inflammatory bowel disease; gluten-sensitive enteropathy;
 autoimmune disease; immune-mediated skin disease; allergic disease;
 immunological disease; transplantation associated disease;
 graft rejection; graft-versus-host-disease.

OS Homo sapiens.

PN WO200053758-A2.

PD 14-SEP-2000.

PF 02-MAR-2000; 2000WO-US05841.

XX 08-MAR-1999; 99WO-US05028.

XX 10-MAR-1999; 99US-0123618.

XX 12-MAR-1999; 99US-0123957.

XX 23-MAR-1999; 99US-0125775.

XX 12-APR-1999; 99US-0128849.

XX 20-APR-1999; 99WO-US08615.

XX 28-APR-1999; 99US-0131445.

XX 04-MAY-1999; 99US-0133371.

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PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.

```

(GENTH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

XX Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX MPI: 2000-572271/53.

XX N-PSDB: AAC58579.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

Claim 33; Fig 2; 309pp; English.

The present invention describes sixty four human PRO proteins which can
 be used in the treatment of immune related diseases. The human PRO
 proteins, anti-PRO antibodies, agonists and antagonists are useful for
 treating and diagnosing immune related disorders. The disorders are
 selected from systemic lupus erythematosus, rheumatoid arthritis,
 osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
 systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 immune-mediated renal disease, demyelinating diseases of the central
 and peripheral nervous systems, hepatobiliary diseases, inflammatory
 bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 autoimmune or immune-mediated skin diseases, allergic diseases,
 immunological diseases of the lung, and transplantation associated
 diseases including graft rejection and graft-versus-host-disease.
 AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 sequences given in the exemplification of the present invention.

SQ Sequence 345 AA:

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Query Match      99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 8.9e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSLEGLLVTSALAGORGTQAESNLSSKFOFSSNKEDONGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHITPRNTVLVWRLVAVEENWIOITFDERGLEDPEDDICKYDFVEVEEPSDGTIL 120
Db 61 PRPHITPRNTVLVWRLVAVEENWIOITFDERGLEDPEDDICKYDFVEVEEPSDGTIL 120
QY 121 GRMGSGTVFGKOISKGNQIRIRFVSDEYFPSPFCIHYNIVMPOFTEAVSPSVLPSSA 180
Db 121 GRMGSGTVFGKOISKGNQIRIRFVSDEYFPSPFCIHYNIVMPOFTEAVSPSVLPSSA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFFGRRKSRVDLNL 240
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFFGRRKSRVDLNL 240
QY 241 LTEEVRLYSCTPRNFSYSIREELKRTDTIFWPGCLVYKRCGGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRLYSCTPRNFSYSIREELKRTDTIFWPGCLVYKRCGGNCACCLHNCNECQVPSK 300
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Db 301 VTKKYHEVLQRPKTVGVLHKSILTVALHHEHEDCVCRCSTGG 345
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Search completed: April 29, 2003, 09:05:43
Job time : 34.5 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:08:16 ; Search time 26.5 seconds
(without alignments)
1043.199 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858
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Total number of hits satisfying chosen parameters: 301932

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications-AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1858	100.0	345	9	US-10-086-623-32
3	1858	100.0	345	9	US-10-260-539-32
4	1858	100.0	345	10	US-09-818-943-1
5	1851	99.6	345	9	US-09-978-295A-488
6	1851	99.6	345	9	US-09-978-697-488
7	1851	99.6	345	9	US-09-978-192A-488
8	1851	99.6	345	9	US-10-139-583-2
9	1851	99.6	345	9	US-09-999-832A-488
10	1851	99.6	345	9	US-09-878-189-488
11	1851	99.6	345	9	US-10-028-072-286
12	1851	99.6	345	9	US-10-121-049-286
13	1851	99.6	345	9	US-10-123-904-286
14	1851	99.6	345	9	US-10-140-470-286
15	1851	99.6	345	9	US-09-976-753-6
16	1851	99.6	345	9	US-10-175-746-286
17	1851	99.6	345	9	US-10-176-918-286
18	1851	99.6	345	9	US-10-176-921-286
19	1851	99.6	345	9	US-10-103-197-4

20	1851	99.6	345	9	US-10-137-865-286	Sequence 286, App
21	1851	99.6	345	9	US-10-140-474-286	Sequence 286, App
22	1851	99.6	345	9	US-10-142-431-286	Sequence 286, App
23	1851	99.6	345	9	US-10-143-114-286	Sequence 286, App
24	1851	99.6	345	9	US-10-140-002-286	Sequence 286, App
25	1851	99.6	345	9	US-09-978-608A-488	Sequence 286, App
26	1851	99.6	345	9	US-10-142-419-286	Sequence 286, App
27	1851	99.6	345	9	US-09-978-191A-488	Sequence 286, App
28	1851	99.6	345	9	US-09-978-403A-488	Sequence 286, App
29	1851	99.6	345	9	US-09-878-564A-488	Sequence 286, App
30	1851	99.6	345	9	US-09-978-585A-488	Sequence 286, App
31	1851	99.6	345	9	US-10-017-081A-488	Sequence 286, App
32	1851	99.6	345	9	US-10-123-262-286	Sequence 286, App
33	1851	99.6	345	9	US-10-142-423-286	Sequence 286, App
34	1851	99.6	345	9	US-09-978-824-488	Sequence 286, App
35	1851	99.6	345	9	US-09-981-915A-488	Sequence 286, App
36	1851	99.6	345	9	US-09-999-833A-488	Sequence 286, App
37	1851	99.6	345	9	US-10-121-050-286	Sequence 286, App
38	1851	99.6	345	9	US-10-141-755-286	Sequence 286, App
39	1851	99.6	345	9	US-10-167-749-488	Sequence 286, App
40	1851	99.6	345	9	US-09-918-585A-488	Sequence 286, App
41	1851	99.6	345	9	US-10-143-032-286	Sequence 286, App
42	1851	99.6	345	9	US-09-978-423A-488	Sequence 286, App
43	1851	99.6	345	9	US-10-013-921A-488	Sequence 286, App
44	1851	99.6	345	9	US-10-123-108-286	Sequence 286, App
45	1851	99.6	345	9	US-10-123-236-286	Sequence 286, App

ALIGNMENTS

RESULT 1

US-09-852-209A-3

Sequence 3, Application US/09852209A

Patent No. US20020164687A1

GENERAL INFORMATION:

APPLICANT: ERIKSSON, ULF

APPLICANT: AASE, Karin

APPLICANT: LEE, Xuri

APPLICANT: FONTEN, Annica

APPLICANT: DUFELO, Marko

APPLICANT: ALITALO, Kari

APPLICANT: OESTMAN, Anne

APPLICANT: HELDIN, Carl-Henrik

APPLICANT: BETSHOLTZ, Christer

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING

FILE REFERENCE: THEREFOR, AND USES THEREOF

CURRENT APPLICATION NUMBER: 09-410349-Eriksson et al-1064-44740

CURRENT FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: 09/410,349

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 60/110,749

PRIOR FILING DATE: 1998-12-03

PRIOR APPLICATION NUMBER: 60/113,002

PRIOR FILING DATE: 1998-12-18

PRIOR APPLICATION NUMBER: 60/135,426

PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: 60/144,022

PRIOR FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 345

TYPE: PRT

ORGANISM: Homo sapiens

US-09-852-209A-3

Query Match 100.0%; Score 1858; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.6e-161;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GRMGSGTVPGKOISKNOIRIRFVSDYFPSEPGFCIHNIYMPQTEAVSPVLPPSA 180
Db 121 GRMGSGTVPGKOISKNOIRIRFVSDYFPSEPGFCIHNIYMPQTEAVSPVLPPSA 180
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Db 181 LPDLNNATTAFTSTLEDLIRYLEPERWOLDLBYRPTMQLGKAFVGRKSRVDNL 240
QY 241 LEEVRLYSTCPNFSYSIREELKRTDTIFMPCGLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LEEVRLYSTCPNFSYSIREELKRTDTIFMPCGLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKHEVLOLRPKTGVGRGLHKSITDVALHHEBCDCVCRGSGTG 345
Db 301 VTKKHEVLOLRPKTGVGRGLHKSITDVALHHEBCDCVCRGSGTG 345
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RESULT 2
US-10-086-623-32
; Sequence 32, Application US/10086623
; Patent No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES TH
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-086-623-32
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Query Match 100.0%; Score 1858; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 2,6e-161;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 GRMGSGTVPGKOISKNOIRIRFVSDYFPSEPGFCIHNIYMPQTEAVSPVLPPSA 180
QY 181 LPDLNNATTAFTSTLEDLIRYLEPERWOLDLBYRPTMQLGKAFVGRKSRVDNL 240
Db 181 LPDLNNATTAFTSTLEDLIRYLEPERWOLDLBYRPTMQLGKAFVGRKSRVDNL 240
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Db 241 LEEVRLYSTCPNFSYSIREELKRTDTIFMPCGLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKHEVLOLRPKTGVGRGLHKSITDVALHHEBCDCVCRGSGTG 345
Db 301 VTKKHEVLOLRPKTGVGRGLHKSITDVALHHEBCDCVCRGSGTG 345
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RESULT 3
US-10-260-539-32
; Sequence 32, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-260-539-32
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Query Match 100.0%; Score 1858; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 2,6e-161;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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;; PRIOR APPLICATION NUMBER: 60/079689
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;; PRIOR FILING DATE: 1998-03-27
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSLLFGLLVTSALAGORRGTOAESNLSSKFQFSSNKEQNGVQDPQHRITTVSTNGSIHS 60
QY 61 PRPHPTVPRNTVTVWVRVVAEENVMWVQLTFDERFGLEDPEDDICXKDFVVEEPPSGTTL 120
DB 61 PRPHPTVPRNTVTVWVRVVAEENVMWVQLTFDERFGLEDPEDDICXKDFVVEEPPSGTTL 120
QY 121 GRWGSQTVPGKQTSKGNQIRIRFVSDVEYFPPSEPGCIHYNIMVQFTFAVSPSVLPSPA 180

Db 121 GRWGSCTVPGKQISKGNQIRIFVSDYPPSPGFCIHYNIVMPQTEAVSPSVLEPPSA 180
Qy 181 LPDLNNATATSTLEDDLRYLEPERWOLDLIVRPTMQLLGGKAFVGRKSRVDNL 240
Db 181 LPDLNNATATSTLEDDLRYLEPERWOLDLIVRPTMQLLGGKAFVGRKSRVDNL 240
Qy 241 LTEEVRLYSTPRNFVSYSINEELKRTDTIFWPGCLLVKRCGNCACCLAHNCNCCVPSK 300
Db 241 LTEEVRLYSTPRNFVSYSINEELKRTDTIFWPGCLLVKRCGNCACCLAHNCNCCVPSK 300
Qy 301 VTKKHEVLDLRKPTGVRCGLHKSITDVALHHEHCCDCVCRGSGTG 345
Db 301 VTKKHEVLDLRKPTGVRCGLHKSITDVALHHEHCCDCVCRGSGTG 345

RESULT 6
US-09-978-697-488
Sequence 488, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFGLLLVTSALAGRGQOAESNLSSKFOFSSNKQONGVQDPQHRITTVTSNGSIHS 60
Db 1 MSFGLLLVTSALAGRGQOAESNLSSKFOFSSNKQONGVQDPQHRITTVTSNGSIHS 60
QY 61 PREPHTYPRNTVLVWRLVAEENWIIQTFDERGLEDPEDDICKYQFVEEPEPSDGTIL 120
Db 61 PREPHTYPRNTVLVWRLVAEENWIIQTFDERGLEDPEDDICKYQFVEEPEPSDGTIL 120
QY 121 GRMGSGTVPGKOISKNOIRIRFVSDPEPSEPCFIHNIYVOPTEAVSPSLPPSA 180
Db 121 GRMGSGTVPGKOISKNOIRIRFVSDPEPSEPCFIHNIYVOPTEAVSPSLPPSA 180
QY 181 LPDDLNNATTAFTLEDLIRYLEPERWQDLEDLYRPTWOLGKARVFGKRSYVDLNL 240
Db 181 LPDDLNNATTAFTLEDLIRYLEPERWQDLEDLYRPTWOLGKARVFGKRSYVDLNL 240
QY 241 LTEEVRILYSCTPRNFVSIVRELRKRTDTIFMPGCLLVKRCGNCACCLHNCNECQVPSK 300
Db 241 LTEEVRILYSCTPRNFVSIVRELRKRTDTIFMPGCLLVKRCGNCACCLHNCNECQVPSK 300
QY 301 VTKKYHEVQLRPKTVGRLHKSLLTDVALEHHEBCDCVCRGSTG 345
Db 301 VTKKYHEVQLRPKTVGRLHKSLLTDVALEHHEBCDCVCRGSTG 345

RESULT 7
US-09-78-192A-488
Sequence 488, Application US/09978192A
Patent No. US2002017753A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Geritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kljavan, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC9
;; CURRENT APPLICATION NUMBER: US/09/978,192A
;; PRIOR FILING DATE: 2001-10-15
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311

[illegible]

;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLLTSALAGRGQTQAESNLSSKFOFSSNKEDQNGVODPQHRITITVSTNGSIHS 60
DB 1 MSLEGLLLTSALAGRGQTQAESNLSSKFOFSSNKEDQNGVODPQHRITITVSTNGSIHS 60
QY 61 PRPHPTPRNTVLVWRLVAEENWVLTQTFDERGLEDPEDDICKYDFVEVEEESDGTIL 120
DB 61 PRPHPTPRNTVLVWRLVAEENWVLTQTFDERGLEDPEDDICKYDFVEVEEESDGTIL 120
QY 121 GRMGSGTVPGKOISKNOQIRIRFVSDEYFPPSEFGCIHNIYMPQTEAVSPVLPPSA 180
DB 121 GRMGSGTVPGKOISKNOQIRIRFVSDEYFPPSEFGCIHNIYMPQTEAVSPVLPPSA 180
QY 181 LPDLNNAITASTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSVVDLNL 240
DB 181 LPDLNNAITASTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSVVDLNL 240
QY 241 LTFEVRLYSCTPRNFSVSTIEELKRTDTIMPGLLYKRCGGNACCLHNCNCCQVPSK 300
DB 241 LTFEVRLYSCTPRNFSVSTIEELKRTDTIMPGLLYKRCGGNACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLQLRPTGVGRLHKSITDVALHHEECDCVCGSTG 345
DB 301 VTKKYHEVLQLRPTGVGRLHKSITDVALHHEECDCVCGSTG 345

RESULT 8
US-10-139-583-2
; Sequence 2, Application US/10139583
; Patent No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGR3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-583-2

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLLTSALAGRGQTQAESNLSSKFOFSSNKEDQNGVODPQHRITITVSTNGSIHS 60

DB 1 MSLEGLLLTSALAGRGQTQAESNLSSKFOFSSNKEDQNGVODPQHRITITVSTNGSIHS 60
QY 61 PRPHPTPRNTVLVWRLVAEENWVLTQTFDERGLEDPEDDICKYDFVEVEEESDGTIL 120
DB 61 PRPHPTPRNTVLVWRLVAEENWVLTQTFDERGLEDPEDDICKYDFVEVEEESDGTIL 120
QY 121 GRMGSGTVPGKOISKNOQIRIRFVSDEYFPPSEFGCIHNIYMPQTEAVSPVLPPSA 180
DB 121 GRMGSGTVPGKOISKNOQIRIRFVSDEYFPPSEFGCIHNIYMPQTEAVSPVLPPSA 180
QY 181 LPDLNNAITASTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSVVDLNL 240
DB 181 LPDLNNAITASTLEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSVVDLNL 240
QY 241 LTFEVRLYSCTPRNFSVSTIEELKRTDTIMPGLLYKRCGGNACCLHNCNCCQVPSK 300
DB 241 LTFEVRLYSCTPRNFSVSTIEELKRTDTIMPGLLYKRCGGNACCLHNCNCCQVPSK 300
QY 301 VTKKYHEVLQLRPTGVGRLHKSITDVALHHEECDCVCGSTG 345
DB 301 VTKKYHEVLQLRPTGVGRLHKSITDVALHHEECDCVCGSTG 345

RESULT 9
US-09-999-832A-488
; Sequence 488, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltson, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James J.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10

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PRIOR APPLICATION NUMBER:	60/081838
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081838

[illegible]

PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLVTSALAGQRRGTOAESNLSSKRFQSSNKEQNGVQDPQHRITVTSNGSIHS 60
D 1 MSLEGLLVTSALAGQRRGTOAESNLSSKRFQSSNKEQNGVQDPQHRITVTSNGSIHS 60
QY 61 PRPHYTPRNTVWRLVAVENWVQLTDERGLEDPEDDICKYDFVEEESDGTIL 120
D 61 PRPHYTPRNTVWRLVAVENWVQLTDERGLEDPEDDICKYDFVEEESDGTIL 120
QY 121 GRMGSGTVGKQISKNQIRIRFVSDYFSPGFCIHYNIVMPQFTFAVSPVLPPSA 180
D 121 GRMGSGTVGKQISKNQIRIRFVSDYFSPGFCIHYNIVMPQFTFAVSPVLPPSA 180
QY 181 LPDLNNATIAFSTEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSFVVDLNL 240
D 181 LPDLNNATIAFSTEDLIRYLEPERWQDLEDLYRPTWQLGKAFVFGKRSFVVDLNL 240
QY 241 LTFEVRILYSCPRNFVSIREELKRTDTIFWPGLLYKRCGGNACCLHNCNEQCVPSPK 300
D 241 LTFEVRILYSCPRNFVSIREELKRTDTIFWPGLLYKRCGGNACCLHNCNEQCVPSPK 300
QY 301 VTKKHEVLQLRPKTGVGLHKSITDVALEHHECDVCVCRSGTG 345
D 301 VTKKHEVLQLRPKTGVGLHKSITDVALEHHECDVCVCRSGTG 345

RESULT 10
US-09-978-189-488
Sequence 488, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: F2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,189

CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

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Query Match          99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,le-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSLEGLLVTSALAGRGTOAESNLSSKFOFSSNKQONGVODPOHERITVSTNGSIHS 60
QY 61 PREPHTYPRNTVLVWRLVAEENWVLIQLTFDERFGLDEDEDICRYDFVEVEPSDGTLL 120
DB 61 PREPHTYPRNTVLVWRLVAEENWVLIQLTFDERFGLDEDEDICRYDFVEVEPSDGTLL 120
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DB 121 GWCSSGTVPGKQISKGNQIRIRFVSDEFPSPEPGCHINYIMQFTEAVSPVLPESA 180
QY 181 LPDLNNAITAFSTLEDIRLPEPRMOLDLDTLRPTWOLLGKAFVGRKSRVVDLNL 240
DB 181 LPDLNNAITAFSTLEDIRLPEPRMOLDLDTLRPTWOLLGKAFVGRKSRVVDLNL 240
QY 241 LEEVRLVSCPTPRNFSVSIREELKRTDITFWPGCLLVKRCGNACACLNHCOCVPSK 300
DB 241 LEEVRLVSCPTPRNFSVSIREELKRTDITFWPGCLLVKRCGNACACLNHCOCVPSK 300
QY 301 VTKKYHEVLIQRPKTGVRLKSLTDVALEHHEECDCVCRSGTG 345
DB 301 VTKKYHEVLIQRPKTGVRLKSLTDVALEHHEECDCVCRSGTG 345

```

```

RESULT 11
US-10-028-072-286
; Sequence 286, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:

```

FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026

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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 19/98-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

```

Query Match 99.6%; Score 1851; DB 9; Length 345;
 Best Local Similarity 99.4%; Pred. No. 1.1e-160; Indels 0; Gaps 0;

```

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLLVTSALAGROGTOAESNLSSKFOFSSNKEONGVODPOHERITVTSNGSIHS 60
DB 1 MSIFGLLLTSALAGROGTOAESNLSSKFOFSSNKEONGVODPOHERITVTSNGSIHS 60

QY 61 PREPHTYPRNTVLYWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTLL 120
DB 61 PREPHTYPRNTVLYWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTLL 120

QY 121 GRWCGSGTYPGKOISGNOIRIRFVSDEYFPSPGFCIHYNIMPOFTEAVSPSVLPSPA 180
DB 121 GRWCGSGTYPGKOISGNOIRIRFVSDEYFPSPGFCIHYNIMPOFTEAVSPSVLPSPA 180

QY 181 LPDLNNMTAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNMTAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVGRKSRVVDNL 240

QY 241 LEEVRLYSTPRNFSVSIREELKRTDTIFWPGCLLYKRCGNCACCLHNCNCCQVPSK 300
DB 241 LEEVRLYSTPRNFSVSIREELKRTDTIFWPGCLLYKRCGNCACCLHNCNCCQVPSK 300

QY 301 VTKKYEVLQLRPKTVGRGLHKSLLTDVALEHHECCDCVCRGSTGG 345
DB 301 VTKKYEVLQLRPKTVGRGLHKSLLTDVALEHHECCDCVCRGSTGG 345

```

RESULT 12

```

US-10-121-049-286
; Sequence 286, Application US/10121049
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen

```

```

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; PRIOR APPLICATION: removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 286
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-286

```

Query Match 99.6%; Score 1851; DB 9; Length 345;
 Best Local Similarity 99.4%; Pred. No. 1.1e-160; Indels 0; Gaps 0;

```

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLLVTSALAGROGTOAESNLSSKFOFSSNKEONGVODPOHERITVTSNGSIHS 60
DB 1 MSIFGLLLTSALAGROGTOAESNLSSKFOFSSNKEONGVODPOHERITVTSNGSIHS 60

QY 61 PREPHTYPRNTVLYWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTLL 120
DB 61 PREPHTYPRNTVLYWRLVAEENWMIQLTFDERFGLEDEDDICKYDFVEVEPSDGTLL 120

QY 121 GRWCGSGTYPGKOISGNOIRIRFVSDEYFPSPGFCIHYNIMPOFTEAVSPSVLPSPA 180
DB 121 GRWCGSGTYPGKOISGNOIRIRFVSDEYFPSPGFCIHYNIMPOFTEAVSPSVLPSPA 180

QY 181 LPDLNNMTAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVGRKSRVVDNL 240
DB 181 LPDLNNMTAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVGRKSRVVDNL 240

QY 241 LEEVRLYSTPRNFSVSIREELKRTDTIFWPGCLLYKRCGNCACCLHNCNCCQVPSK 300
DB 241 LEEVRLYSTPRNFSVSIREELKRTDTIFWPGCLLYKRCGNCACCLHNCNCCQVPSK 300

QY 301 VTKKYEVLQLRPKTVGRGLHKSLLTDVALEHHECCDCVCRGSTGG 345
DB 301 VTKKYEVLQLRPKTVGRGLHKSLLTDVALEHHECCDCVCRGSTGG 345

```

RESULT 13

```

US-10-123-904-286
; Sequence 286, Application US/10123904
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel

```

```

; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 286
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-123-904-286

Query Match          99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLTVTSALAGORGTQAESNLSSKFOFSSNKQNGVODPQHRITITVSTNGSIHS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSLEGLLLTSALAGOGTQAESNLSSKFOFSSNKQNGVODPQHRITITVSTNGSIHS 60

QY 61 PREPHTYPRNTVLVWRLVAEENWVIOITFDERFGLEDPEDDICKYDFVEVEEESDGTIL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PREPHTYPRNTVLVWRLVAEENWVIOITFDERFGLEDPEDDICKYDFVEVEEESDGTIL 120

QY 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPEPFCIHNIYVPOFTEAVSPSVLPSSA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPEPFCIHNIYVPOFTEAVSPSVLPSSA 180

QY 181 LPDLNNAITAEFTEDLIRYLEPERWOLDLEDLYRPTWQLGKAFVFGKRSKRVLDNL 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LPDLNNAITAEFTEDLIRYLEPERWOLDLEDLYRPTWQLGKAFVFGKRSKRVLDNL 240

QY 241 LTEEVRLYSCTPRNFVSISIEELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQVPSK 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LTEEVRLYSCTPRNFVSISIEELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKKYEVLQLRPTGVGRLHKSITDVALHHEBCDCVCGSGTGG 345
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 VTKKYEVLQLRPTGVGRLHKSITDVALHHEBCDCVCGSGTGG 345

RESULT 14
US-10-140-470-286
; Sequence 286, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION removed - See Palm or File Wrapper
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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 286
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-140-470-286

Query Match          99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLEGLLTVTSALAGORGTQAESNLSSKFOFSSNKQNGVODPQHRITITVSTNGSIHS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSLEGLLLTSALAGOGTQAESNLSSKFOFSSNKQNGVODPQHRITITVSTNGSIHS 60

QY 61 PREPHTYPRNTVLVWRLVAEENWVIOITFDERFGLEDPEDDICKYDFVEVEEESDGTIL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PREPHTYPRNTVLVWRLVAEENWVIOITFDERFGLEDPEDDICKYDFVEVEEESDGTIL 120

QY 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPEPFCIHNIYVPOFTEAVSPSVLPSSA 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GRMGSGTVGKQISKNOIRIRFVSDEYFPEPFCIHNIYVPOFTEAVSPSVLPSSA 180

QY 181 LPDLNNAITAEFTEDLIRYLEPERWOLDLEDLYRPTWQLGKAFVFGKRSKRVLDNL 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LPDLNNAITAEFTEDLIRYLEPERWOLDLEDLYRPTWQLGKAFVFGKRSKRVLDNL 240

QY 241 LTEEVRLYSCTPRNFVSISIEELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQVPSK 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LTEEVRLYSCTPRNFVSISIEELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKKYEVLQLRPTGVGRLHKSITDVALHHEBCDCVCGSGTGG 345
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 VTKKYEVLQLRPTGVGRLHKSITDVALHHEBCDCVCGSGTGG 345

RESULT 15
US-09-796-753-6
; Sequence 6, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION removed: 09/471,179
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; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 6
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-6
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```

Query Match          99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1,1e-160;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSALAGRGSTQAESNLSSKQFSSNKQNGVODPOHERITTVSTNGSIHS 60
Db 1 MSIFGLLVTSALAGRGSTQAESNLSSKQFSSNKQNGVODPOHERITTVSTNGSIHS 60

QY 61 PRPHTYPRNTVLVWRLVAEENWMIQLTFDERFGLDEPEDDICKYDFVEEPPSDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAEENWMIQLTFDERFGLDEPEDDICKYDFVEEPPSDGTIL 120

QY 121 GRWCGGTVPQKQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPSSA 180
Db 121 GRWCGGTVPQKQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPSVLPSSA 180

QY 181 LPLDLNNAITAFSTLEDLIRYLEPFRWOLDLDRPTWOLGKAFVGRKSRVVDNL 240
Db 181 LPLDLNNAITAFSTLEDLIRYLEPFRWOLDLDRPTWOLGKAFVGRKSRVVDNL 240

QY 241 LTEEVRLYCTPRNFSVSIREELKRTDTIFWPGCLVYKRCGNCACCLHNCNCCQVPSK 300
Db 241 LTEEVRLYCTPRNFSVSIREELKRTDTIFWPGCLVYKRCGNCACCLHNCNCCQVPSK 300

QY 301 VTKKYHEVQLRPTKGVRLHSLTDVALEHHHECCDCVCGSTGG 345
Db 301 VTKKYHEVQLRPTKGVRLHSLTDVALEHHHECCDCVCGSTGG 345
```

Search completed: April 29, 2003, 09:16:55
Job time : 27.5 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:03:41 ; Search time 55 Seconds
(without alignments)
1292.477 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858

Sequence: 1 MSIFGLLVTSALAGORGT.....DVALEHHECDVCVCGSTGG 345

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organella:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-virus:*
- 16: sp-bacteriap:*
- 17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	100.0	345	4 Q9NRAL	Q9NRAL homo sapien
2	1851	99.6	345	4 Q9UL22	Q9UL22 homo sapien
3	1664	89.6	345	11 Q9QY71	Q9QY71 mus musculus
4	1646	88.6	345	11 Q9EOX6	Q9EOX6 rattus norv
5	1635	88.0	345	11 Q9JH8	Q9JH8 mus musculus
6	1614	86.9	345	13 Q9JH8	Q9JH8 mus musculus
7	741.5	39.9	370	4 Q9GZP0	Q9GZP0 homo sapien
8	740.5	39.9	364	4 Q9BWS	Q9BWS homo sapien
9	737.5	39.7	370	11 Q9Z517	Q9Z517 mus musculus
10	736	39.6	370	11 Q9EQT1	Q9EQT1 rattus norv
11	645	34.7	290	11 Q9DIL8	Q9DIL8 mus musculus
12	190.5	10.3	923	13 Q8OFX6	Q8OFX6 brachydanio
13	183	9.8	3623	4 Q50494	Q50494 homo sapien
14	182	9.8	691	13 Q57658	Q57658 gallus galli
15	180	9.7	34	11 Q9JH4	Q9JH4 mus musculus
16	176	9.5	977	13 Q91925	Q91925 xenopus lae

17	176	9.5	3623	11 Q70244	Q70244 rattus norv
18	172	9.3	1012	11 Q9WVM6	Q9WVM6 mus musculus
19	171	9.2	735	13 Q57381	Q57381 xenopus lae
20	171	9.2	926	4 Q9UQ00	Q9UQ00 homo sapien
21	171	9.2	1015	4 Q9Y617	Q9Y617 homo sapien
22	169	9.1	241	11 Q92135	Q92135 rattus norv
23	165.5	8.9	555	4 Q8QZV7	Q8QZV7 mus musculus
24	164.5	8.9	555	4 Q9H2E2	Q9H2E2 homo sapien
25	164.5	8.9	901	4 Q9H2E4	Q9H2E4 homo sapien
26	164.5	8.9	901	4 Q9H2D5	Q9H2D5 homo sapien
27	164.5	8.9	906	4 Q9H2E3	Q9H2E3 homo sapien
28	164.5	8.9	906	4 Q9H2D4	Q9H2D4 homo sapien
29	163.5	8.8	921	11 Q9QX38	Q9QX38 rattus norv
30	163.5	8.8	3620	6 Q9UW53	Q9UW53 carls famll
31	158.5	8.5	609	4 Q96190	Q96190 homo sapien
32	158.5	8.5	644	4 Q961H5	Q961H5 homo sapien
33	158.5	8.5	704	4 Q9H2E1	Q9H2E1 homo sapien
34	157.5	8.5	919	13 Q8UVRO	Q8UVRO gallus galli
35	157.5	8.5	936	13 Q8UVQ9	Q8UVQ9 gallus galli
36	157	8.4	1008	13 Q9DER7	Q9DER7 gallus galli
37	153	8.2	415	4 Q9UKZ9	Q9UKZ9 homo sapien
38	153	8.2	1019	13 Q57382	Q57382 xenopus lae
39	151.5	8.2	326	11 Q91ZE4	Q91ZE4 rattus norv
40	151	8.1	276	4 Q9BRH3	Q9BRH3 homo sapien
41	149	8.0	1013	4 Q43897	Q43897 homo sapien
42	149	8.0	1013	4 Q9NOS4	Q9NOS4 homo sapien
43	148.5	8.0	414	11 Q9CX06	Q9CX06 mus musculus
44	148.5	8.0	414	11 Q8R4W6	Q8R4W6 mus musculus
45	148	8.0	358	13 Q57434	Q57434 fuigu rubrip

ALIGNMENTS

RESULT 1

Q9NRAL PRELIMINARY: PRT; 345 AA.

AC Q9NRAL: 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Platelet-derived growth factor C.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LUNG;

RA MEDLINE=20268201; PubMed=10806482;

RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Utecla M., Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P., Betscholtz C., Heidin C.-H., Alltalo K., Ostman A., Eriksson U.;

RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-receptor";

RT Nat. Cell Biol. 2:302-309(2000).

CC - SIMILARITY: CONTAINS 1 CUB DOMAIN.

DR EMBL: AF244813; AAF80597.1; -

DR InterPro: IPR000859; CUB_domain.

DR InterPro: IPR000072; PD_growth_factor.

DR Pfam: PF00431; CUB; 1.

DR Pfam: PF00341; PDGF; 1.

DR SMART: SM00042; CUB; 1.

DR SMART: SM00141; PDGF; 1.

DR PROSITE: PS01180; CUB; 1.

DR PROSITE: PS50278; PDGF_2; 1.

SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 100.0%; Score 1858; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 9.5e-170;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLVTSALAGORGTQAEISNLSKRFQSSNKEQNGVDPQHERITVSTNSINS 60

Db	1	MSLFGLLLVTSALAGQRGRGTGAESNLSPKQFSSNKQNGVQDPQHRRITTVTSNGSIHS	60
Qy	61	PRFRPTTYPRNTVLYWRLYAVEENWITQLTDERGEGLEDPEDDICKYDFVEEEDSDGTIL	120
Db	61	PRFRPTTYPRNTVLYWRLYAVEENWITQLTDERGEGLEDPEDDICKYDFVEEEDSDGTIL	120
Qy	121	GRMGCSGVVPCKQKJISKGQIIRFVSDSEYPPSEPGFCHININYPQTEAVSPSVLPESA	180
Db	121	GRMGCSGVVPCKQKJISKGQIIRFVSDSEYPPSEPGFCHININYPQTEAVSPSVLPESA	180
Qy	181	LPRLDLNNAITAFSTLEDLIRYLEPEREMQDLDELYRPTQQLGKAFVFGRSKRVVDNL	240
Db	181	LPRLDLNNAITAFSTLEDLIRYLEPEREMQDLDELYRPTQQLGKAFVFGRSKRVVDNL	240
Qy	241	LTEEYRLTSCIPRNFSVISIREELKRTDTIPWPCCLLVKKRCGGNACCCAHNCNECQVPSK	300
Db	241	LTEEYRLTSCIPRNFSVISIREELKRTDTIPWPCCLLVKKRCGGNACCCAHNCNECQVPSK	300
Qy	301	VTKKYNHEVLDLRPTGVGRLKSLTDVALENHNECCDVCVGSSNGG	345
Db	301	VTKKYNHEVLDLRPTGVGRLKSLTDVALENHNECCDVCVGSSNGG	345

RESULT 2			
ID	Q9UL22	PRELIMINARY:	PRT: 345 AA.
AC	Q9UL22;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Secretory growth factor-like protein FALLOUTIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).		
GN	HSCDGF OR PDGFC.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxId:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=UTERUS;		
RA	Tsai Y.J., Lee R.K.K., Lin S.P.;		
RT	"Falloutin, a novel growth factor like gene identified in human uterus."		
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BRAIN;		
RA	MEDLINE=20317014; PubMed=10858496;		
RX	Hanada T., Ui-Tel K., Miyata Y.;		
RT	"A novel gene derived from developing spinal cords, SCDF, is a unique member of the PDGF/VEGF family."		
RL	FEBS Lett. 475:97-102(2000).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21347863; PubMed=11297552;		
RA	Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,		
RA	Hofstetson P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,		
RA	Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;		
RT	"Platelet-derived growth factor C (PDGFC), a Novel Growth Factor That Binds to PDGF alpha and beta Receptor."		
RL	J. Biol. Chem. 276:27406-27414(2001).		
CC	-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.		
CC	EMBL: AF091434; AAF00049.1; -;		
CC	EMBL: AB033831; BAB03266.1; -;		
CC	EMBL: AF260738; AAK51637.1; -;		
DR	InterPro: IPR000859; CUB_domain.		
DR	InterPro: IPR000072; PD_growth_factor.		
DR	Pfam: PF00431; CUB; 1.		
DR	Pfam: PF00341; PDGF; 1.		
DR	SMART: SM00042; CUB; 1.		
DR	SMART: SM00141; PDGF; 1.		
DR	PROSITE: PS01180; CUB; 1.		

DR PROSITE: PS50278; PDGF 2: 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;
Query Match 99.6%; Score 1851; DB 4; Length 345;
Best Local Similarity 99.4%; Pred. No. 4.4e-169;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0.

Qy	1	MSLGLLLVTSALGQRRGTPQAEINSSKQFSSSKRQNGVQPOHRIITVSNNGSIHS	60
Db	1	MSLFGLLLTLSALAGQNGQNGQAEINSSSKQFSSSKRQNGVQPOHRIITVSNNGSIHS	60
Qy	61	PRPHTYPRNTVLVWRLVAEENWAIQITDEREGLEDPEDDICKYDFVEEBSDGTIL	120
Db	61	PRPHTYPRNTVLVWRLVAEENWAIQITDEREGLEDPEDDICKYDFVEEBSDGTIL	120
Qy	121	GRMGSGSGVPGKQJTSKSNQIRIRFVSDEYFPSEPGFCIHNIYMPQFTEAVSPVLPPSA	180
Db	121	GRMGSGSGVPGKQJTSKSNQIRIRFVSDEYFPSEPGFCIHNIYMPQFTEAVSPVLPPSA	180
Qy	181	LPRLDLLNNAITASTEDDLIRYLEPERKMOLEDLIRPTMQLLGKAPVGRSKSRVVDNL	240
Db	181	LPRLDLLNNAITASTEDDLIRYLEPERKMOLEDLIRPTMQLLGKAPVGRSKSRVVDNL	240
Qy	241	LTEEVRLYSCTPRNFVSYSIREELKRTBTJIMPGGCLTVKRCGAGCACALHNCNEQCPVSK	300
Db	241	LTEEVRLYSCTPRNFVSYSIREELKRTDTJIMPGGCLTVKRCGAGCACALHNCNEQCPVSK	300
Qy	301	VTKKRYHEVLQIRPTQYVGRGLKSLTVDALHNHEECDCVCGSGTGG	345
Db	301	VTKKRYHEVLQIRPTQYVGRGLKSLTVDALHNHEECDCVCGSGTGG	345

RESULT 3	090Y71	PRELIMINARY:	PRT:	345 AA.
ID	090Y71			
AC	090Y71;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	Fallotectin (Platelet-derived growth factor C).			
GN	PDGFC.			
OS	Mus musculus (Mouse).			
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=OVARY;			
RA	Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;			
RT	"cDNA cloning of fallotectin from mouse ovary";			
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN=C57BL/6J;			
RA	Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,			
RT	Gilbertson D., West J., O'Hara P.J.;			
RT	"Platelet-derived growth factor C (PDGFC-C), a novel growth factor that			
RL	binds to PDGF alpha receptor.";			
CC	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.			
DR	EMBL: AF117608; AAF22516.1; -;			
DR	EMBL: AF266467; AAK58566.1; -;			
DR	MGI: MG1:1859631; PdGfc.			
DR	InterPro: IPR000859; CUB_domain.			
DR	InterPro: IPR000072; PD_growth_factor.			
DR	Pfam: PF00431; CUB. 1.			
DR	Pfam: PF00341; PDGF. 1.			
DR	SMART: SM00042; CUB. 1.			
DR	SMART: SM0141; PDGF. 1.			
DR	PROSITE: PS01180; CUB. 1.			
DR	PROSITE: PS00278; PDGF_2. 1.			
QO	SEQUENCE 345 AA; 38741 MW; 3A58A1F701B94EA2 CRC64;			

	Query Match	89.6%: Score 1664; DB 11; Length 345;
	Best Local Similarity 86.7%: Pred. No. 3.8e-151;	
	Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;	
QY	1 MSLFGLILVTSALGQRGRTQAEISNLSSKRFQSSMKKEONGVODPOHERIITVSTGSIHS 60	
Db	1 MLLGLITLTSALAGQRTGRTAESHLSKSLQISSKEDQNGVODPHHERVITISGSIHS 60	
QY	61 PRPFITVPRNTVLVWRLVAEENWITQLTFDERGLEDEDDICKYDVEVEPSDGTLL 120	
Db	61 PKFPIYTRNNVLVWRLVAEDENWITQLTFDERGLEDEDDICKYDVEVEEPPSDGSVL 120	
QY	121 GRMGCGSGVPPGKQISKQNIIRIRFVSDSEYPSPEPFCIHYNIVMOPFEAVSPSLRPSA 180	
Db	121 GRMGCGSGVPPGKQISKGNHIRIRFVSDSEYPSPEPFCIHYSITIMQVETLTPSVLPBSS 180	
QY	181 LPLDLLNNAITAFSTLEDLIRYLEPERMQQLDELDYRPTWQLLGKAFYGRKSRVLDLNL 240	
Db	181 LSLDLLNNAVTAFTSLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSSKYVNLNL 240	
QY	241 LTEYRLVLSCTPRNFSVSIREDLKTDTITFWPGCLLYVRGCGNACACCLHNCNECCVPBK 300	
Db	241 LKEEYKLYLSCTPRNFSVSIREDLKTDTITFWPGCLLYVRGCGNACACCLHNCNECCVPBK 300	
QY	301 VTKKUYHEVLDLRPTGVGLHKSLLDVALLHNNBECDCVCRSGTG 345	
Db	301 VTKKUYHEVLDLRPTGVGLHKSLLDVALLHNNBECDCVCRSGTAGG 345	

[illegible]

QY	121	GRMGSGVPEPKQJSTKSGNQIIRFVPSQDEYFPSEPGFCHININIVMPQTEAVSPVLPSSA	180
QY	121	GRMGSGVPEPKQJSTKSGNQIIRFVPSQDEYFPSEPGFCHININIVMPQTEAVSPVLPSSA <td>180</td>	180
Db	121	GRMGSGVPEPKQJSTKSGNHIRFVPSDEYFPSEPGFCHINISIMPVUTETTTSPVLPSSA	180
QY	181	LPLDLLNNAITAFSTLEDDLYRELEPERKQDLEDDLYRPTQQLGKAFVFGKRSKVDYLN	240
Db	181	LSLDLNLNNAITAFSTVEELIRFLEPRDKQIDDDSLYKPTPLGKARLYGKSKSAVNLN	240
QY	241	LTEEYRLVLSCTPRNFVSISIRELKRDTITIMPQGLLVKRCGGNACCLHNCNECQVPSK	300
Db	241	LKEEYKLVLSCTPRNFVSISIRELKRDTITIMPQGLLVKRCGGNACCLHNCNECQVPSK	300
QY	301	VTKKYUHEVLDLRPTGVRGLSKSLTDVALEHNEECDDCVSGSTGG	345
Db	301	VTKKYUHEVLDLRPTGVRGLSKSLTDVALEHNEECDDCVSGMNTGG	345

ID	09JHVB	PRELIMINARY:	PRF:	345 AA.
AC	09JHVB:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Platelet-derived growth factor C.			
GN	PDGFC.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SWISS-WEBSTER/NIH;			
KX	MEDLINE=20417814; PubMed=10960785;			
RA	Ding H., Wu X., Kim I., Tam P.P., Koh G.Y., Nagy A.;			
RT	"The mouse Pdgfr gene: dynamic expression in embryonic tissues during			
RT	organogenesis.";			
RL	Mech. Dev. 96:209-213(2000).			
CC	-I- SIMILARITY: CONTAINS 1 CUB DOMAIN.			
DR	EMBL; AF286725; AAF91483.1; -.			
DR	MGI; MGI:1859631; Pdgfr.			
DR	InterPro; IPR000859; CUB_domain.			
DR	InterPro; IPR000072; PD_growth_factor.			
DR	Pfam; PF00431; CUB: 1.			
DR	SMART; SM00042; CUB: 1.			
DR	SMART; SM00141; PDGF: 1.			
DR	PROSITE; PS01180; CUB: 1.			
DR	PROSITE; PS50278; PDGF-2; 1.			
SO	SEQUENCE 345 AA; 38886 MW; PA146BED6D362FE CRC64;			
Query Match 88.0%; Score 1635; DB 11; Length 345;				
Best Local Similarity 85.5%; Pred. No. 2.3e-148;				
Matches 295; Conservative 28; Mismatches 22; Indels 0; Gaps 0;				
QY	1 MSFLLLVLTALAGRGCTGAESNLSSKFPSSKKEONGVDDPQHERITVSTNGSIHS 60			
DB	1 MLLGLLLLTSLAGQRTGTRAESNLSSKQLSSDKEDGVDDPHERKVTISGNGSIHS 60			
QY	61 PRFPTPRNTVTLVWRLVAVEENWVLTLPDEFERGLEPDEDDICKYDVEVEEPPSDGTL 120			
DB	61 PKFPTVDRNNVTLVWRLVAVDENVRTQLTFPERFLEPDEDDICKYDVEVEEPPSDGTVL 120			
QY	121 GRWGSGGVPEGQKSIKGNQIRIRFVSDSEYFSEPGFCIHYNWFOFTLEAVSPVLPESA 180			
DB	121 GRWGSEFVPEKQTSKGNHIRIRFVSDSEYFSEPGFCIHYSIMPOVETETSPVLPSS 180			
QY	181 LPLDLLNAATFASTLEDLIRLPEERMOQLDELDYRPTWOLGKAFEGGRSRVDDL 240			
DB	181 LSLDLLNAATFASTLEELIRLPEDRKQVDDLSLYKFTWOLGKAFYLVKSKVNNL 240			
QY	241 LTEEVRLVSCPTPRNFVSIRRELKRTDTIFWPGCLVRCGNCACCLAHNCECCVPSK 300			

Db 241 LKEEKLXSCRRPNFSVSIREDLKRTRDTRFPGGLLKRCGGNACCLHMCNEQCVPRK 300

QY 301 VTKKYHEULDRPKTVGNGLKSLTDVALENNHECDVCRCSTGG 345

Db 301 VTKKYHEULDRPKTVGNGLKSLTDVALENNHECDVCRCSTGG 345

RESULT 6 ,
Q91946
ID Q91946 PRELIMINARY; PRT; 345 AA.

DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Spinal cord-derived growth factor.
CU

OS *Gallus gallus* (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC *Gallus*.
 OK NCBI_TaxID=9031;

RC STRAIN=WHITE LEGHORN; TISSUE=SPINAL CORD;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tel K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SODGF, is a unique
RT member of the PDGF/MGF family. ";
RT nmap1044 425-02-10232000.

```
CC      -l SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR      EMBL; AB033829; BABO3265.1; "-  
DR      InterPro; IPR000859; CUB_domain.  
DR      InterPro; IPR000072; PD_growth_factor.  
DR      Pfam; PF00431; CUB; 1.  
DR      Pfam; PF00341; PDGF; 1.  
DR      SMART; SMO0042; CUB; 1.  
DR      SMART; SMO0141; PDGF; 1.  
DR      PROSITE; PS01180; CUB; 1.  
DR      PROSITE; P55028; PDGF_2; 1.  
SQ      SEQUENCE   345 AA;    38940 MW;          97ACEA992BF5128C CRC64
```

Query Match	86.9%	Score 1614	DB 13	Length 345
Best Local Similarity	83.8%	Pred No. 2.3e-146		
Matches 289	Conservative 31	Mismatches 25	Indels 0	Gaps 0

QY 1 MSLEGLLVTSALAGORGTQAESNLSKSFQESSNKEQNVDPDHERITVSTNGSIHS 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 MLLGILLTSLAAGRHRGAAESDSLKSFSFQAKKEQNVDPDHEKITVTSNGSIHS 60

```
QY      61 PREPHATYPRNTVLVWRLVAVEENWMIQITFDEFRGLEDEDDICKYDFVEVEEPPSDGTL 1200
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 PKFPHATYPRNTVLVWRLVAVEENWMIQITFDEFRGLEDEDDICKYDFVEVEEPPSDGTVL 1200
```

```
QY      121 GRMGSGTVEGKQISKGNQIRIRFVSDEYFPSEGEFCIHNIWMQFTAVSPSLPPSA 1800
        ||||| :||:|||||:|||||:|||||:::|| ||| ||||
Db      121 GRMGSSSVSRQISKGNQIRIRFVSDEYFPSEQGFCIHNTLLVPHHTAPSPSLPPSA 1800
```

```
QY 181 LPDLNNATFASTEDLIRLPERKQDLEDLYRPWQLGCAVFGRKSRVVDNL 2400
    |||:||||: |||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 181 LPPLVNNAAVGSTVEELIRLEPDRQDLEDLYRPWQLGKAYIHGKSRVVDNL 2400
```

```
OY      241 LTEEKLRYLSCTPRNFSVSIRELTKRTDIFWPGLLVKKGCGGNACCLHNCNECCQVPSK 3000
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | : |
Db      241 LKEEVLRYLSCTPRNFSVSLREBLKRTDIFWPLCLLVKKGCGGNACCHQNENECCQLPTK 3000
```

QY	301	VTKRYHEVLQRPKVTGVRGLHKSLTDVALENHECCDCVARGSTGC	345
		:::	:::
Db	301	VTKRYHEVLQRPKRGVRLHKSLTDVPLENHECCDCVAKGNSEG	345

RESULT 7
Q9GZP0
ID Q9GZP0 PRELIMINARY; PRT; 370 AA.

AC OEG2PO: 01-MAR-2001 (Tremblrel, 16, Created)
 DT 01-MAR-2001 (Tremblrel, 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel, 21, Last annotation update)
 DE SPINAL-CORD-derived growth factor-B (MSP036) (IRIS-expressed growth factor long form) (Platelet-derived growth factor D).
 DE HSCDGF-B OR IEGF OR PDGFD

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RA Hamada T., Uti-Tel K., Imaki J., Miyata Y.:
RT "Molecular Cloning of SCDFG-B, a Novel Growth Factor Homologous to
RT SCDFG/PDGF-C/Intenotin"
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
121

RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RC TISSUE=IRIS;
RA Wistow G.;
RT "Iris-expressed Growth Factor (IEGF)".
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases
[4]

RA Bergsten E., Untela M., Li X., Pietras K., Ostman A., Heldin C.H.,
RA Allitalo K., Eriksson U.;
"PDGF-D is a specific, protease-activated ligand for the PDGF beta
RT receptor.";
RL Nat. Cell Biol. 3:512-516(2001).

RA Laroche W.J., Jeffers M., McDonald W.F., Chikluru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Deegler L.B., Ridgman B., Shinkels J.,
RA Shinkels R.A., Rothberg J.M., Lichenslein H.S.;
RT "PDGF D": A Novel Protease-Activated Growth Factor. ";

```
DR. EMBL; AF113216; AAC39287.1; -.
DR. EMBL; AY025717; AAK20081.1; -.
DR. EMBL; AF336337; AAK56136.1; -.
DR. EMBL; AF335584; AAK38840.1; -.
DR. InterPro; IPR000859; CUB_domain.
InterPro; IPR000859; CUB_domain.
```

DR SMART; SM00141; PDGE; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGE_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
SO SEQUENCE 370 AA; 42848 MW; D367F485E7BB7674 CRR64

Query Match	39.9%	Score 741.5;	DB 4	Length 370;
Best Local Similarity	43.68%	Pred. No. 1.2e-62;		
Matches 159;	Conservative 59;	Mismatches 114;	Indels 33;	Gaps 10;

Oy 3 LFGLLVTSALAGQRRGTQAESNLSSKFQFSNN---KEONGYVD-PQHERRITVSINGSI 568
 :|::||::||| | || ::
Dd 5 IFVVTLICANFCSCRDTSATPQSASIKALARNANLRDESNHLLTDLYRREDTIQVKNGYV 644

[illegible]

ID	Q9BMV5	PRELIMINARY:	PRT:	364 AA.
AC	Q9BMV5			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Iris-expressed growth factor short form.			
GN	IEGF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC-	TISSUE=IRIS;			
RA	Wistow G.;			
RT	"Iris-expressed Growth Factor (IEGF).";			
RL	Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.			
CC	-I- SIMILARITY: CONTAINS 1 CUB DOMAIN.			
DR	EMBL: AY027518; AAK20082.1; -			
DR	InterPro: IPR000859; CUB_domain.			
DR	InterPro: IPR000072; PD_growth_factor.			
DR	InterPro: IPR000531; TonB_boxc.			
DR	Pfam: PF00431; CUB; 1.			
DR	SMART: SM00042; CUB; 1.			
DR	SMART: SM00141; PDGF; 1.			
DR	PROSITE: PS01180; CUB; 1.			
DR	PROSITE: PS00278; PDGF_2; 1.			
DR	PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN.1.			
DR	SEQUENCE 364 AA: 42166 MW; 249C35EBDDAE9AC CRC64;			
Query Match	39.9%; Score 740.5; DB 4; Length 364;			
Best Local Similarity	43.2%; Pred. No. 1.4e-62;			
Matches 156; Conservative 61; Mismatches 113; Indels 31; Gaps				
QY	3 LFGLLVYSALAGQRGQDAESNLSSKPFSSNNKEDNGYQDPQHEHITIVSTNGSIHSR 62			
DB	5 IIVYLLICNFCSCSDTSATPQSAISKALRNANLRDDLY--RRETIQVKNKGYYQSPR 62			
QY	63 PPHYTPRNTVLWLVAAVEENWVIOLTDEPREGLEDPEDDICKYFVEVEEPSDGF--IL 120			
DB	63 FPNSTVPRNLLWLRHLS-QENTRIQLVFNQNGLEAEANDICRYDVEVEDLSSTIIR 121			
QY	121 GWMCGSGIVPGQKISKNGDIRLEVSDXYFPSEPGCFHYINIVMPQTEAV----- 171			
DB	122 GWMCGSGIVPGQKISKNGDIRLEVSDXYFPSEPGCFHYINIVMPQTEAV----- 180			

Oy	172	-----SPSYLPSPALPDLIDNNATGASFLDEEYLYLEBBEROGLDEEDLYRRTWQ	221
Db	181	TSSISGVSYNSPSVTDPT-LIADLADKKIAEFDTVEDLLKYFPNESWOEDLENMYLDTPR	239
Oy	222	LIGKAFYFGRRSRVVDILLTEERFLXSCPPRNFSVISIRELKRTDIFMPGCLLYKRCG	281
Db	240	YRGHSY-HDRSK-VDDRLDLNDAKRKRSPPRNYSVAIRREKLANYVFFPRCLLYVRGC	297
Oy	282	GNCACCLHNCNECOCVPBSKVTKKHVEYLQRP--KTGVGRGLIKSLTDVALIEHHESCDV	338
Db	298	GNCGGIVNMNRSTCNSGKTVKKHYEVLQEPHGIIKRGRGRAKTMALVIDLIIDHNERDCI	357
Oy	339	I	
Db	358	C 358	

RESULT	ID	PRELIMINARY:	PRT:	370 AA.
092517	092517			
AC	092517			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Platelet-derived growth factor D.			
GN	PDGFD.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RI	[1]			
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C;			
RX	MEDLINE=21231380; PubMed=11331882;			
RA	Lacrochelle W.J., Jeffers M., McDonald W.F., Chiklaku R.A.,			
RA	Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,			
RA	Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,			
RA	Shinkets R.A., Rothberg J.M., Lieberstein H.S.;			
RT	"PDGF D, A Novel Protease-Activated Growth Factor.";			
RL	Nat. Cell Biol. 3:517-521(2001).			
DR	EMBL; AF335583; AAK38839.1; -			
DR	MGD; MGI:1919035; Pdfigd.			
DR	InterPro; IPR000859; CUB_domain.			
DR	InterPro; IPR00072; PD_growth_factor.			
DR	Pfam; PF00431; CUB. 1.			
DR	SMART; SMO0141; PDGF. 1.			
DR	PROSITE; PS01180; CUB. 1.			
DR	PROSITE; PS0278; PDGF_2. 1.			
SO	SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;			

[illegible]

OY 295 QCVPSKYTKYHEVLOLRP---KTGVRGLHKSITLVDLHNEECDCVC 339
 DB 317 TCSSGKTKYKHYHEVLRPEFGHFKRGAKNMALVDIOLDHNERCJCIC 364

RESULT 10

Q9EQT1

AC O9EQT1 PRELIMINARY; PRT; 370 AA.

DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Spinal-cord derived growth factor-B.
 GN RSCDGF-B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21092670; PubMed=11162582;
 RA Hamada T., Ue-Tel K., Imaki J., Miyata Y.;
 RT Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
 RT SCDF/PDGF-C/fallicotin."
 RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AB052170; BAB19920.1; -;
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS02278; PDGF_2; 1.
 SQ SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BE73 CRC64;

Query Match 39.6%; Score 736; DB 11; Length 370;
 Best Local Similarity 45.6%; Pred. No. 3.9e-62;
 Matches 149; Conservative 57; Mismatches 93; Indels 28; Gaps 9;

OY 37 EQNGVDP-FOHERITVSTNGSHSPRPHTYPRNTLVLRVAVENWVIQTLFDERFG 95
 DB 42 ESNLTLTLDRENDIRYTGCHGVSPRPNSYPRNLTLRLHS-QEKTQLQLFDDHOG 100
 OY 96 LEDEDDICKDFEVEEPESDGT--ILGRMGSGCTVPGKQISKNOJRIREFVSVEYEPSE 153
 DB 101 LEEAENDICRDFEVEEEDVSSSTVVRGRCGKHEIPRITSRTNOIKITFOSDYFAK 160
 OY 154 PGFCIHNYIV---MPQTEAV-----SPSVLPSPALPLDLLNNAITAFST 195
 DB 161 PGFIYYSFVEDFQPEAASEINMESVTSFSGVSYHSPSVW-DSTLVADALDKAIAFEDT 219
 OY 196 LEDLIRLLEPERWQDLEDLIRPTWQLLGAFAVGRKSRVVDLNLLEVRVLSCTPRNF 255
 DB 220 VEDLLKFNPAWQDLENLIMPTDPRYGRSRY-HERKSK-VDLDRDLDDVKKRYSCPRNH 277
 OY 256 SVSIRELEKRTDIFWPGCCLVVRGCGNACCLHNECOCVPSKYTKYHEVLOLRP-- 313
 DB 278 SVNIRELEKRTNAVFPRCLLVORCGNGCGTLNKKSCSSGSKYTKYHEVLRPEFGH 337
 OY 314 -KTGVRGLHKSITLVDLHNEECDCVC 339
 DB 338 FKRGRGAKNMALVDIOLDHNERCJCIC 364

RESULT 11

Q9DIL8

AC O9DIL8 PRELIMINARY; PRT; 290 AA.

DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE 1110003109Rik protein.
 GN PDEGD OR 1110003109Rik.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC SRRAIN-C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawal J., Shinnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arawaka T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudl J., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AK003359; BAB22735.1; -;
 DR MGD: MGI:1919035; Pdfigd.
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS02278; PDGF_2; 1.
 SQ SEQUENCE 290 AA; 33425 MW; 14214509E6717D4B CRC64;

Query Match 34.7%; Score 645; DB 11; Length 290;
 Best Local Similarity 45.4%; Pred. No. 1.5e-53;
 Matches 128; Conservative 48; Mismatches 80; Indels 26; Gaps 6;

OY 81 EENNWLTLFDERGLEDPPDDICKYDFEVEEPESDGT--ILGRMGSGCTVPGKQISKCN 138
 DB 6 QEKTRIQLSFDHOGLEAENDICRDFEVEEVESSSTVVRGRCGKHEIPRITSRTN 65
 OY 139 QIRIRFVSDEFSEPGFCIHNYIVMPQTEAV-----SPSVLPSPA 180
 DB 66 QIKRTKFSDDYFAKRPFKIYISFVEDFQPEAASETWESVTSFSGVSHRSISITPT- 124
 OY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGAFAVGRKSRVVDLNL 240
 DB 125 LTADALDKTVAEEFTVVDLKHENPVSMDLENLIDTDPHYGRSRY-HNRKSK-VDLDR 182
 OY 241 LTBELVRLYSCPRNFVSISIEELKRTDIFWPGCCLVVRGCGNACCLHNECOCVPSK 300
 DB 183 LNDVKKRYSCPRNHSVNLBELEKRTNAVFPRCLLVORCGNGCGCTVWKKSCSSGSK 242
 OY 301 VTKKYHEVLOLRP---KTGVRGLHKSITLVDLHNEECDCVC 339
 DB 243 TVKKYHEVLRPEFGHFKRGAKNMALVDIOLDHNERCJCIC 284

RESULT 12

Q8QFX6

AC Q8QFX6 PRELIMINARY; PRT; 923 AA.

DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Neupophilin-1.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
 RT "Neupophilin-1 is required for normal vascular development and is a
 RT mediator of VEGF-dependent angiogenesis in zebrafish."
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY064213; AAL40862.1;
 SQ SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;

Query Match 10.3%; Score 190.5; DB 13; Length 923;
 Best Local Similarity 27.6%; Pred. No. 2.6e-09;
 Matches 66; Conservative 29; Mismatches 95; Indels 49; Gaps 8;

OY 5 GLLVTSALAGORRGQASNLSSKQFSSNKGQNGVDPQHERLITTSNGSIHSRPP 64
 DB 12 GFLIYSAKNDKCGDN-----IRITSANYLTSPGTP 43
 OY 65 HPTPTVTLVRLVAEENWVQLTFDERFGLDEPDICKYDFVEVEPSD--GTILGR 122
 DB 44 VSYPSQKCIWITARGPQRILINPNPHDLEDR---CKDYVEVRGVDENGGLVCK 100
 OY 123 WCGSGVPGKQSKNQIRVSDYFSPSEGCYHYNIWMP-----QFTAVSPSVL 176
 DB 101 YCGK-TAPSPVVSQGNLFKPVSD-YETHGAGFSIRYELFKTGPCSRFTFS--SSGV 156
 OY 177 PSALPLDLLNNAITAFSTLEDLIRYLEPERMQDLEDYRPTWOLLGKAFVGRKSRV 235
 DB 157 KSPGPEKTPNNLDCITFMFAPKMSIIVLEFESFELEPDTQP-----PAGVFCRIIDL 209

RESULT 13
 060494 PRELIMINARY: PRT: 3623 AA.
 ID 060494: 096R09; PRT: 3623 AA.
 AC 060494: 096R09; PRT: 3623 AA.
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-JAN-1999 (TREMBlrel. 09, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Intrinsic factor-B12 receptor precursor (Intrinsic factor-vitamin B12 receptor).
 GN CUBN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97476251; PubMed-9334227;
 RA Birn H., Verroust P.J., Nexø E., Jacobsen C.,
 RA Christensen E.I., Moestrup S.K.;
 RT "Characterization of an epithelial approximately 460-kDa protein that
 RT facilitates endocytosis of intrinsic factor-vitamin B12 and binds
 RT receptor-associated protein."
 RT J. Biol. Chem. 272:26497-26504(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-98241400; PubMed-9572993;
 RA Kozyrak J.R., Kristiansen M., Sijlhaug A., Hansen C., Jacobsen C.,
 RA Tommerup N., Verroust P.J., Moestrup S.K.;
 RT "The human intrinsic factor-vitamin B12 receptor, cubilin: molecular
 RT characterization and chromosomal mapping of the gene to 10p within the
 RT autosomal recessive megaloblastic anemia (MGA1) region."
 RN [3]
 RP SEQUENCE OF 130-3623 FROM N.A.
 RA Amthoff M., Brady S., Verroust P.J., Moestrup S.K., Krahe R.;
 RT "The genomic structure of the human CUBN gene encoding cubilin, the

RT Intrinsic factor-vitamin B12 receptor."
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 26 CUB DOMAINS.
 DR EMBL; AF034611; AAC82612.1;
 DR EMBL; AF243129; AAK61830.1;
 DR EMBL; AF243083; AAK61830.1; JOINED.
 DR EMBL; AF243084; AAK61830.1; JOINED.
 DR EMBL; AF243085; AAK61830.1; JOINED.
 DR EMBL; AF243086; AAK61830.1; JOINED.
 DR EMBL; AF243087; AAK61830.1; JOINED.
 DR EMBL; AF243088; AAK61830.1; JOINED.
 DR EMBL; AF243089; AAK61830.1; JOINED.
 DR EMBL; AF243090; AAK61830.1; JOINED.
 DR EMBL; AF243091; AAK61830.1; JOINED.
 DR EMBL; AF243092; AAK61830.1; JOINED.
 DR EMBL; AF243093; AAK61830.1; JOINED.
 DR EMBL; AF243094; AAK61830.1; JOINED.
 DR EMBL; AF243095; AAK61830.1; JOINED.
 DR EMBL; AF243096; AAK61830.1; JOINED.
 DR EMBL; AF243097; AAK61830.1; JOINED.
 DR EMBL; AF243098; AAK61830.1; JOINED.
 DR EMBL; AF243099; AAK61830.1; JOINED.
 DR EMBL; AF243100; AAK61830.1; JOINED.
 DR EMBL; AF243101; AAK61830.1; JOINED.
 DR EMBL; AF243102; AAK61830.1; JOINED.
 DR EMBL; AF243103; AAK61830.1; JOINED.
 DR EMBL; AF243104; AAK61830.1; JOINED.
 DR EMBL; AF243105; AAK61830.1; JOINED.
 DR EMBL; AF243106; AAK61830.1; JOINED.
 DR EMBL; AF243107; AAK61830.1; JOINED.
 DR EMBL; AF243108; AAK61830.1; JOINED.
 DR EMBL; AF243109; AAK61830.1; JOINED.
 DR EMBL; AF243110; AAK61830.1; JOINED.
 DR EMBL; AF243111; AAK61830.1; JOINED.
 DR EMBL; AF243112; AAK61830.1; JOINED.
 DR EMBL; AF243113; AAK61830.1; JOINED.
 DR EMBL; AF243114; AAK61830.1; JOINED.
 DR EMBL; AF243115; AAK61830.1; JOINED.
 DR EMBL; AF243116; AAK61830.1; JOINED.
 DR EMBL; AF243117; AAK61830.1; JOINED.
 DR EMBL; AF243118; AAK61830.1; JOINED.
 DR EMBL; AF243119; AAK61830.1; JOINED.
 DR EMBL; AF243120; AAK61830.1; JOINED.
 DR EMBL; AF243121; AAK61830.1; JOINED.
 DR EMBL; AF243122; AAK61830.1; JOINED.
 DR EMBL; AF243123; AAK61830.1; JOINED.
 DR EMBL; AF243124; AAK61830.1; JOINED.
 DR EMBL; AF243125; AAK61830.1; JOINED.
 DR EMBL; AF243126; AAK61830.1; JOINED.
 DR EMBL; AF243127; AAK61830.1; JOINED.
 DR EMBL; AF243128; AAK61830.1; JOINED.
 DR HSSP; P35555; 1EMN.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR Pfam: PF000431; CUB; 27.
 DR Pfam: PF00008; EGF; 5.
 DR SMART; SM00042; CUB; 26.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00001; EGF_like; 5.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01180; CUB; 27.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_4.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR KEGG; K04480; EGF-like domain; Glycoprotein; Hydroxylation;
 KW Receptor; Repeat; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 3623 POTENTIAL.
 SQ SEQUENCE 3623 AA; 398991 MW; A91AVCEA5348651 CRC64;
 FT

```

Query Match          9.8%; Score 183; DB 4; Length 3623;
Best Local Similarity 26.2%; Pred. No. 8.6e-08;
Matches 96; Conservative 42; Mismatches 139; Indels 90; Gaps 23;

QY 19 GTAESNLSKRFQ-----SSKKEONG-----VDDPQHERITIVSTGSHSPFPFH 65
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 892 GTDIPSTFTSVNLYVTFFVKSSSTENHGFMAKPSADLACGELITTEST-CTIOSPCHPN 950

QY 66 TYPRTNVLVRLVAVEENWMIQLTFDERFGLEDDEDDICKYDFEVEPEPSDGTILGRCG 125
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 951 VYRHGICHTHIL-VQDNHILHLMF-ETFLHERHYN--CTNDVLEVDYDTSLSGRRCG 1006

QY 126 SGTVPGQKQSKGNOIRIRFVSDVEFPSEPGFCHYNIV-----MPOFTEAVSPSVLPSPS 179
   ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1007 K-SIPPELTSSGNSLMVFTDSDLAYE-GFLINVEALISATACLDQYTDGLGFTSP-- 1062

QY 180 ALPDLILNNMITAFTSTEDLIRYIEPERMOLDEDLYR---PTMQLLKGKAFVGRKRRV 236
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1063 ----NFSNN-----YFNNW-----ECIRIRIVTGOQLTAVHFTNFSLEBAI 1099

QY 237 DLNLTRE--EVR-----LY--SCTPRNFSYSIREELK-RFDTI-----FW 271
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1100 G-NYTFPLEIRDGGYKSKPLIGFYGSNLPPTIISHSNKMLKFKSDQIDTRGFSAYW 1158

QY 272 PGCLLVKRCGCNACCLHNCNCCVPSKYTKYHE--VLQLRPKTGVKQLHKSITDVA 328
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1159 DGS--STGCCGN---LTTSSGFTISPNYPMYPYHSEGCYWLKSSHG-SAFELEFRDFH 1211

QY 329 LEHHEEC 335
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1212 LEHHPNC 1218

RESULT 14
ID 057658 PRELIMINARY; PRT: 691 AA.
AC 057658;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Bone morphogenetic protein 1 (Fragment).
GN BMP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20267865; Pubmed=10806368;
RA Reynolds S.D., Zhang D., Puzas J.E., O'Keefe R.J., Rosler R.N.,
RA Reynolds P.R.;
RT Cloning of the chick BMP1/Tolloid cDNA and expression in skeletal
RT tissues.;
RL Gene 248:233-243(2000).
CC - SIMILARITY: CONTAINS 3 CUB DOMAINS.
DR EMBL: U75331; AAC02259.1; -
DR HSSP: P00736; IAP0.
DR MEROPS: M12.005; -
DR InterPro: IPR001506; Astacin.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000130; Zn_metallopeptidase.
DR Pfam: PF01400; Astacin, 1.
DR Pfam: PF00431; CUB; 3.
DR Pfam: PF00008; EGF; 1.
DR PRINTS: PR00480; ASTACIN.
DR SMART: SM00042; CUB; 3.
DR SMART: SM00179; EGF_CA_1.
DR SMART: SM00235; ZMGC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.

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DR PROSITE: PS01180; CUB; 3.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA_1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
FT NON_TER
FT TER
SQ SEQUENCE 691 AA; 77843 MW; 01245982B8DC8F28 CRC64;

Query Match          9.8%; Score 182; DB 13; Length 691;
Best Local Similarity 38.5%; Pred. No. 1.2e-08;
Matches 50; Conservative 20; Mismatches 48; Indels 12; Gaps 7;

QY 55 NGSINSPRFHTYPRNTVLVRLVAVEENWMIQLTFDERFGLEDDEDDICKYDFEVEE- 113
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 560 NGSISSPGPRDYPNKHCVWLVAPTQ-YRISLRFD---FFPEEGNDVCYDFEVRSG 615

QY 114 -PSDGTILGRCWCSGYTPGQKQSKGNOIRIRFVSDVEFPSEPGFCHYNIVMPOFTEAVS 172
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 616 LTLADSKLHGKFCGGG-LPGAITSQYNNMRYEPRSYNTV-AKRGKAHF--FSEKQOQL 670

QY 173 PSVLPSPALP 182
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 671 PPQIPP-ALP 679

RESULT 15
ID 099JM4 PRELIMINARY; PRT: 34 AA.
AC 099JM4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Similar to platelet-derived growth factor, C polypeptide
DE (Fragment).
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC006027; AAH06027.1; -
DR MGD: MGI:1859631; Pdgcfc.
FT NON_TER
FT TER
SQ SEQUENCE 34 AA; 3618 MW; F4AB6A3A414AED9E CRC64;

Query Match          9.7%; Score 180; DB 11; Length 34;
Best Local Similarity 91.2%; Pred. No. 3.3e-10;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 312 RPRTGVRLHKSITDVALLEHHEEDCYCRGSTG 345
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1 RPRTGVRLHKSITDVALLEHHEEDCYCRGNAG 34

```

Search completed: April 29, 2003, 09:08:08
Job time : 59 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:04:11 ; Search time 15.5 Seconds

(without alignments)
2139.766 Million cell updates/sec

Title: US-09-818-943-1

Perfect score: 1858

Sequence: 1 MSRLGLLVTSALAGQRGRT.....DVALEHHECDQVCRGSGTG 345

Scoring table:

BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	742.5	40.0	370	2 JC7591	spinal cord-derive
2	736	38.6	370	2 JC7592	spinal cord-derive
3	183	9.8	3623	2 T09456	intrinsic factor-B
4	181.5	9.8	730	1 BMH01	procollagen C-endo
5	179.5	9.7	927	1 J00948	A5 antigen precurs
6	176	9.5	707	2 JC2218	procollagen C-endo
7	176	9.5	3623	2 T08818	intrinsic factor-B
8	173	9.3	823	1 A58788	procollagen C-endo
9	169	9.1	986	1 B58788	procollagen C-endo
10	169	9.1	991	2 A49540	procollagen C-endo
11	154	8.3	449	2 A55362	procollagen I C-pr
12	148.5	8.0	1057	1 A39288	dorsal-ventral pat
13	143.5	7.7	686	1 A59271	Ra-reactive factor
14	139.5	7.5	1070	2 T31069	colloid-BMP-1 like
15	138.5	7.5	597	2 S71352	metalloproteinase
16	138	7.4	695	1 C1HURB	complement subcomp
17	137.5	7.4	709	1 I54763	Ra-reactive factor
18	137.5	7.4	1524	2 T30337	polypeptide - Afri
19	133	7.2	1594	2 T30549	hensin - rabbit
20	132	7.1	419	2 S68207	vascular endotheli
21	130.5	7.0	1464	2 S58984	development protei
22	128	6.9	402	2 T30018	procollagen I C-pr
23	127.5	6.9	767	2 T30018	hypothetical prote
24	127.5	6.9	3871	2 T22812	hypothetical prote
25	125	6.7	198	2 A47035	platelet-derived g
26	123.5	6.6	277	2 A41735	hyaluronate-bindin
27	123.5	6.6	579	2 JC7629	membrane-type fir12
28	120.5	6.5	245	1 TVCTSS	platelet-derived g
29	120.5	6.5	275	2 JC6506	tumor necrosis fac

30	118.5	6.4	276	2 A47290	TSG-6 homolog PS4
31	114.5	6.2	148	2 D49530	16k vascular endot
32	114.5	6.2	241	1 PFHUG2	platelet-derived g
33	112.5	6.1	200	2 I51551	platelet-derived g
34	112.5	6.1	215	2 S08220	platelet-derived g
35	112.5	6.1	226	2 I51550	platelet-derived g
36	111.5	6.0	319	2 I51569	platelet-derived g
37	110.5	5.9	2403	2 A59386	UVS-2 protein - Af
38	110	5.9	166	2 JN0248	sanko - human
39	109	5.9	197	2 S25096	platelet-derived g
40	108.5	5.8	226	1 TVMWSS	platelet-derived g
41	108	5.8	196	2 A37359	PDGF-related trans
42	104.5	5.6	232	2 A41551	platelet-derived g
43	104	5.6	196	2 B28964	vascular endotheli
44	104	5.6	211	1 PFHUG1	platelet-derived g
45	103	5.5	770	2 D89447	protein F57C12.1 f

ALIGNMENTS

RESULT 1

JC7591
spinal cord-derived growth factor-B precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #extl_change 24-Aug-2001
C:Accession: JC7591
R:Hamada, T.; Ul-Tel, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Accession: JC7591
A:Molecule type: DNA
A:Residues: 1-370 <HAM>
A:Cross-references: DDBJ:AB033832
C:Genetics:
A:Gene: scdf-B
F:1-17/Domain: secretory signal sequence #status predicted <Sig>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <Mat>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial g
F:294-308/Region: conserved motif #status predicted

Query Match	Score	Length	DB 2:
Best Local Similarity	43.6%	Pred. No. 9.5e-57;	
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;			
QY 3 LFGLLVTSALAGQRGRTQAEINLSKPFQSSN---KEQNGVOD-PQHERIITVSTNGSI 58			
DB 5 IFVYTLICANFSCSDRTSATPQASIKALNANLNRDESHNLDLYRRDETIOVKGNGYV 64			
QY 59 HSRPHTYTPRNTLVYRLVAEENWVIOITFDERGLEDDPDDICKYDFVEVEPSDGT 118			
DB 65 QSRPFNSYPRNLTITWRILMS-OENRTIOLVFNQGLEAEANDICRYDFVEVEDISETS 123			
QY 119 --ILGRMGSGTVPGKOISGNOIRIRFVSDVEPSPGCHYINVMQFTAV----- 171			
DB 124 TIRGRMCGHKEVPRKRSSTNOIKTFKSDDFVAKPGKITYSL-LEDFQPAASETN 182			
QY 172 -----SPSVLPSPALPLDLNNAATSTEDLDLRYLEPERMQLDELDLYR 217			
DB 183 WESVTSISGSVSNPSVTDPT-LIADALDKRTAIEDTVEDDLKTFNPESMQDLEMYTL 241			
QY 218 PTMQLLGAFAVFRKSRVVDLNLTEBEVRLSCTPRNFSVSIIEELKRDITTPGCLLV 277			
DB 242 DTFPRYGRSY-HSRKSR-VDLIDRLINDAKRYSCTPRYSVNIREELKLANVFEPRCLLV 299			
QY 278 KRGGMGACCLHMCNCGQCVPSVTKKYHEVLQLRP---TGVRGJLKSJLDVALENHEE 334			
DB 300 QRGGMGCGCTVMRSCSTGSKTVKKYHEVLQEPGHLRRGRAKTMAVLDIOLDHNER 359			
QY 335 CDCVC 339			

Db 360 CDCIC 364

RESULT 2

JC7592

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001

C:Accession: J07592

R:Hamada, T.; Ui-Tel, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C

A:Reference number: JC7591; MOID:21092670; PMID:11162582

A:Contents: Fetal brain

A:Accession: J07592

A:Molecule type: mRNA

A:Residues: 1-370 <HAM>

A:Cross-references: DDBJ:AB052170

C:Genetics:

A:Gene: scdGF-B

F:1-17/Domain: secretory signal sequence #status predicted <SIG>

F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>

F:52-170/Region: CUB domain #status predicted

F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial grow

F:294-308/Region: conserved motif #status predicted

Query Match

Best local Similarity 45.6%; Pred. No. 3.5e-56;

Matches 149; Conservative 57; Mismatches 93; Indels 28; Gaps 9;

39.6%; Score 736; DB 2; Length 370;

Query 37 EQNGVOD-PQHERITVSTNGSIHSPRPHTYPRNTLVLRVLAEEENWVLTQTFDERFG 95

Db 42 ESNHFLDYLRDENIRVTGCHVQSPRPNSYPNLLTLRLHS-QEKTRIQLAHQFG 100

Query 96 LEEDPDDICRYDVEVEPEBDGT--ILGRMGSTVPGKQISKGNQIRIRFVSDETPSE 153

Db 101 LEERENDICRYDVEVEPEBDGT--ILGRMGSTVPGKQISKGNQIRIRFVSDETPSE 160

Query 154 PGFCIHNYI--MPQTEAV-----SPVLPSALPLDLLNMTAFST 195

Db 161 PGFKIYTFEDDQPEASLNNESVTSFSGSYHSPSW-DSTLADALDAIAEFD 219

Query 196 LEDLIRLEPERQDLEDLIRPTMQLGKAFVGRKSRVVDLNLTEVRLXSCPTP 255

Db 220 VEDLLKFNPMASODDENLYMDTPRYGRSY-HERKSK-VDDLRLNDVYKRSCTPRNH 277

Query 256 SVSIRELRTKTDIFWPGCLLYKRCGNACCLHNCNCCQVSKYTKKHEVQLRP-- 313

Db 278 SVMLREKLKLTNAVFPRCLLVORCGNCGGTLNMRKSCITSSGKTYKKYHEVLKFE 337

Query 314 -KTGVRGLHKSITDVALEHHECDVC 339

Db 338 FKRRGAKKMAVLDIQLDHHRCDCIC 364

RESULT 3

T09456

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002

C:Accession: T09456

R:Kozyrak, R.; Kristiansen, M.; Slihtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.

Blood 91, 3593-3600, 1998

A:Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz

ion.

A:Reference number: Z16677; MOID:98241400; PMID:9572993

A:Accession: T09456

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-3623 <KOZ>

A:Cross-references: EMBL:AF034611; NID:93929528; PIDN:AAC82612.1; PID:93929529

C:Genetics:

A:Map position: 10p12

C:Superfamily: Intrinsic factor-B12 receptor cubilin; EGF homology
C:Keywords: receptor; vitamin B12 uptake
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F:436-467/Domain: EGF homology <EGF>

Query Match

Best local Similarity 26.2%; Pred. No. 8.3e-07;

Matches 96; Conservative 42; Mismatches 139; Indels 90; Gaps 23;

Query 19

Db 892

Query 66

Db 951

Query 126

Db 1007

Query 180

Db 1063

Query 237

Db 1100

Query 272

Db 1159

Query 329

Db 1212

RESULT 4

BMH01

C:Species: Homo sapiens (man)

C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999

C:Accession: A37278; E58788.

R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, B.; Whitters, M.J.; Kriz, R.W.;

Science 242, 1528-1534, 1998

A:Title: Novel regulators of bone formation: molecular clones and activities.

A:Reference number: A37278; MOID:89072730; PMID:3201241

A:Accession: A37278

A:Molecule type: mRNA

A:Residues: 1-730 <WOZ>

A:Cross-references: GB:M22488; NID:9179499; PIDN:AAA51833.1; PID:9179500

C:Genetics:

A:Gene: GDB:BMH01

A:Map position: 8p21-8p21

C:Function:

A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen t

C:Superfamily: procollagen C-endopeptidase; aspartic homology; C1r/C1s repeat homology

C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication;

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT

F:330-321/Domain: aspartic homology <AST>

F:322-431/Domain: C1r/C1s repeat homology <C1R1>

F:435-544/Domain: C1r/C1s repeat homology <C1R2>

F:551-587/Domain: EGF homology <EGF>

F:591-700/Domain: C1r/C1s repeat homology <C1R3>

F:91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644

F:213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted

F:214/Active site: Glu #status predicted

F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match

Best Local Similarity 37.3%; Pred. No. 1.5e-07;
Matches 50; Conservative 20; Mismatches 47; Indels 17; Gaps 7;

QY 55 NSGHSRPHRYPRNTVLVRLVA-VEENWMIQLFDFERFGLDEPDDEDDICKYDFEVEE 113

Db 599 NGSITSFGMKREYPPNKNICMQLVAPQYRISLQDFEEFTEG-----NDCKYDFEVEVS 653

QY 114 --PSDGTILGRMGSGGVPEPKQISKGNQIRIRFVSDEYFSEFGFCHYINWQFTFNAV 171

Db 654 GLTADSKLHKFCGS-EKPEVITSQYNNMREKSDNTV-SKKGFAHF-----FSEK- 704

QY 172 SPSTLPPSALPLDL 185

Db 705 RPAIQPPRGRPHOL 718

RESULT 5

J00948

A5 antigen precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C:Accession: J00466; J00948

R:Takegi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.

Neuron 7, 295-307, 1991

A:Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology

A:Reference number: J00466; M01D:91337458; PMID:1908252

A:Accession: J00466

A:Molecule type: mRNA

A:Residues: 1-927 <TAK>

A:Cross-references: GB:D10467; GB:D01077; NID:9222962; PIDN:BA01260.1; PID:9222963

A:Experimental source: tadpole, brain

A:Note: this protein has motifs homologous to complement components C1r and C1s and to C

C:comment: This protein is a neuronal cell surface molecule involved in the neuronal rec

C:superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal

C:Keywords: duplication; glycoprotein; transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-927/Product: A5 antigen #status predicted <A5A>

F:27-138/Domain: C1r/C1s repeat homology <C1R1>

F:147-262/Domain: C1r/C1s repeat homology <C1R2>

F:274-424/Domain: discoidin I amino-terminal homology <DN1>

F:430-584/Domain: discoidin I amino-terminal homology <DN2>

F:646-812/Domain: MAM homology <MAM>

F:861-883/Domain: transmembrane #status predicted <TM>

F:150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 9.7%; Score 179.5; DB 1; Length 927;
Matches 55; Conservative 29; Mismatches 73; Indels 17; Gaps 7;

QY 50 ITVSTNSHSRPHRYPRNTVLVRLVA-VEENWMIQLFDFERFGLDEPDDEDDICKYDFV 109

Db 31 IKITSPSYLTSAGYPSHPYSQRCWEMIQAPHYORIMINFNHFDLEDE---CKDYV 87

QY 110 EV--EESPDSTILGRMGSGGVPEPKQISKGNQIRIRFVSDEYFSEFGFCHYINWMP-- 165

Db 88 EVIDGDANQQLGKCYGK-IAPSPLVSTGPSFIRFVSDEYFPG-AGSFIRFVEFETGP 145

QY 166 ----QFTEA--VSPSYLPPSALPLDLNNAITAFSTLEDIRYLEPPERMQDLE 213

Db 146 ECSRNFSTSSNGVLSKSPYKPYNALECYTIIFAPKMQEIV--LEFESFLEAD 197

RESULT 6

JC2218

procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)

N:Alternate names: bone morphogenic protein 1

C:Species: Xenopus laevis (African clawed frog)

C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999

C:Accession: JC2218

R:Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.

Gene 134, 257-261, 1993

A:Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic pr

A:Reference number: JC2218; M01D:94085787; PMID:8262384

A:Accession: JC2218

A:Molecule type: mRNA

A:Residues: 1-707 <MAE>

A:Cross-references: GB:L12249; NID:9406540; PIDN:AA016313.1; PID:9406541

A:Comment: This protein induces ectopic cartilage formation in vivo.

C:Superfamily: procollagen C-endopeptidase; asparagin homology; C1r/C1s repeat homology

C:Keywords: beta-hydroxyasparagine, glycoprotein; hydrolase; metalloproteinase; zinc

F:33-284/Domain: asparagin homology <AST>

F:285-397/Region: complement Ir/Is-like repeat

F:385-394/Domain: C1r/C1s repeat homology <C1R1>

F:398-510/Region: complement Ir/Is-like repeat

F:398-507/Domain: C1r/C1s repeat homology <C1R2>

F:514-550/Domain: EGF homology <EGF>

F:554-666/Region: complement Ir/Is-like repeat

F:554-663/Domain: C1r/C1s repeat homology <C1R3>

F:62,105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted

F:177/Active site: Glu #status predicted

F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match

Best Local Similarity 9.5%; Score 176; DB 2; Length 707;
Matches 45; Conservative 15; Mismatches 36; Indels 8; Gaps 5;

QY 55 NSGHSRPHRYPRNTVLVRLVA-VEENWMIQLFDFERFGLDEPDDEDDICKYDFEVEE- 113

Db 562 NGSITSFGMKREYPPNKNICMQLVAPQYRISLQDFEEFTEGDKYDFEVEVRS 617

QY 114 --PSDGTILGRMGSGGVPEPKQISKGNQIRIRFVSDEYFSEFGFCHYINWQFTFNAV 156

Db 618 LTDSKRLHKFCGS-ELPATTISQYNNMREKSDNTV-SKKG 659

RESULT 7

T08618

Intrinsic factor-B12 receptor CUBILIN precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002

C:Accession: T08618

R:Moestrup, S.K.; Kozyrakl, R.; Kristiansen, M.; Kayesen, J.H.; Rasmussen, H.H.; Braul

J. Biol. Chem. 273, 5235-5242, 1998

A:Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibody

A:Reference number: Z16459; M01D:98148073; PMID:9478979

A:Accession: T08618

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Cross-references: EMBL:AF022247; NID:93834379; PIDN:AAC71661.1; PID:93834380

C:Genetics:

C:Superfamily: Intrinsic factor-B12 receptor cubilin; EGF homology

C:Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membra

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-1623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>

F:133-164/Domain: EGF homology <EGF1>

F:436-467/Domain: EGF homology <EGF2>

Query Match

Best Local Similarity 9.5%; Score 176; DB 2; Length 3623;
Matches 95; Conservative 52; Mismatches 133; Indels 92; Gaps 24;

QY 2 SLFGLLVY--SALAGRGTOAESNLSSKFPSSKNGQVODPOHERITVSTNGSH 59

Db 901 SYVNIILYVTFVKSSSMENRGFTA-----KSSSKLECG-----EVLTAFT--GIIE 944

QY 60 SRPFPHRYPRNTVLVRLVA-VEENWMIQLFDFERFGLDEPDDEDDICKYDFEVEEEDGT 119

Db 945 SPHPHWYPRGVCNTWV--VQNGQLRLTFSS--FLEFHYN--CTNDVLEIYDTAQT 1000

QY 120 LGRMGSGGVPEPKQISKGNQIRIRFVSDEYFSEFGFCHYINWQFTFNAVSP 173

[illegible]

RESULT 8

Procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
 Alternative names: bone morphogenic protein splice form BMP-1/His
 R.Mozney, J.M.; Rosen, V.; Celeste, A.J.; Mitscock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
 Science 242, 1528-1534, 1998
 A:Title: Novel regulators of bone formation: molecular clones and activities.
 A:Reference number: A37278; PMID:89072730; PMID:3201241
 A:Accession: A37278
 A:Molecule type: mRNA
 A:Residues: 1-702, 'EKRALPPRRPHQLKFRVQRNRTPQ' <WOZ>
 A:Cross-references: GB:M22488; NID:9179499; PIDN:AAA51833.1; PID:9179500
 R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
 J. Biol. Chem. 269, 32572-32578, 1994
 A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encod
 A:Reference number: A58788; PMID:95096114; PMID:7798260
 A:Accession: A58788
 A:Molecule type: mRNA
 A:Residues: 703-823 <TRAK>
 A:Cross-references: GB:U35578; NID:9619423; PIDN:AAC41703.1; PID:9619424
 C:Genetics:
 A:Gene: GDB:BMP1; BMP-1
 A:Cross-references: GDB:125203; OMIM:112264
 A:Map position: 8p21-8p21
 C:Function:
 A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type
 C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; E
 C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl
 F.1-22/Domains: signal sequence #status predicted <SIG>
 F.23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
 F.130-321/Domains: astacin homology C<AST>
 F.322-443/Domains: C1r/C1s repeat homology <C1R1>
 F.435-544/Domains: C1r/C1s repeat homology <C1R2>
 F.551-587/Domains: BGF homology <BGF>
 F.591-700/Domains: C1r/C1s repeat homology <C1R3>
 F.738-752/Region: histidine-rich
 F.91, 142, 332, 363, 599/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F.163-319, 185-205, 322-348, 375-397, 435-461, 488-510, 551-563, 559-572, 574-587, 591-617, 644-66
 F.213-217, 223, 272/Binding site: zinc (His, His, His, Tyr) #status predicted
 F.214/Active site: Glu #status predicted
 F.3565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match	9.38;	Score 173;	DB 1;	Length 823;
Best Local Similarity	35.6%;	Pred. No. 9.3e-07;		
Matches	52;	Conservative	19;	Mismatches 49;
			Indels	26;
			Gaps	77;

```

QY 55 NGSIISPREPITYPRNTVLWKRIVA-VEENWMIOTLFDERFGLPEDEDDICKYDFVEEE 113
      ||||| : ||| : : ||| : |||||
Db 599 NGSIISPGWPREYPPNKNCIWGLVAPQYRISLQDFFEIEG-----NDVCKYDFVEVRS 653

```

Oy 114 --PSGTLLGMMGGATVPKQISKGNIRLRFEVDEFFPSPGCIHYNIMVOFTPAV 171
| : : : : | : : : : | : : : : | : : : : |
Db 654 GUTASRKLHGFCGS -EXPEYITISQYNNMRREFKSDNTIV-SKKGRKAIFSVLBSAGDRH 711

Oy 172 S-----PSVL-----PPSAL 181
| : : : : | : : : : | : : : : | : : : : |
Db 712 SHLSGLELLLCPHALVTVPAPPSAL 737

RESULT 9

procollagen candopectidase (EC 3.4.24.19) precursor, tolloid-like splice form
N.alternate names: bone morphogenetic protein 1, tolloid-like splice form
C.Species: Homo sapiens (man)
C.Date: 28-Mar-1998 #sequence_revision 03-Apr-1998 #text_change 16-Jul-1999
C.Accession: A37278; B58788
R.McMurry, J.M.; Rosen, V.; Celeste, A.J.; Mltsock, L.M.; Whitters, M.J.; Kriz, R.W.;
Science 242, 1528-1534, 1988
A.Title: Novel regulators of bone formation: molecular clones and activities.
A.Reference number: A37278; MUID:89072730; PMID:3201241
A.Accession: A37278
A.Molecule type: mRNA
A.Residues: 1-702; 'EKRPALQPRGRPHQLKFRVQKRNRTPO' <NO2>
A.Cross-references: GB:M2248; NID:9179499; PIDN:AAA5183.1; PID:9179500
R.Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A.Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mtld) are en-
A.Reference number: A58788; MUID:95096114; PMID:7798260
A.Accession: B58788
A.Molecule type: mRNA
A.Residues: 703-986 <PAK>
A.Cross-references: GB:J5279; NID:9619860; PIDN:AAC41710.1; PID:9619861

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Query March          9.1%; Score 169; DB 1; Length 986;  
Best Local Similarity 39.4%; Pred. No. 2.6e-06;  
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;
```

OY 55 NGSIHSPREPHPTYPENFLVWRLVA-VVENWIQLTPDEREGLEDPEDDICKYDFVEVEE 113
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 599 NGSIISSPGMPREYPPNKKNCIMQLVAPFTQYRISLQPDFETEGS----NDVCXKIDFEVRS 653

OY 114 --PSSGTTILRGCGSGIVTGPCKOISKGNQIRLRFSDEFFPSPEPCIH Y 160
 |:::|:::|||||:::|:::|:::|:::|:::|:::|:::|:::
Db 654 GTLTADSKLHGKFCGS-EKEPVITSDQYNMNRVEKFEDNTV-SKKCKRAHF 700

RESULT 10
149540

Procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
c1Species: Mus musculus (house mouse)

A::Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-449 <TRK>
A::Cross-references: GB:LI33799; NID:g642907; PIDN:AAA61949.1; PID:g642908
C:Genetics:
A:Gene: GDB:PCOLCE
A::Cross-references: GDB:305468; OMIM:600270
A:Map position: 7q21.3-7q22
C:Superfamily: Clr/Cls repeat homology
C:Keywords: extracellular protein; glycoprotein; pyroglutamic acid
F:1-45/Domain: signal sequence #status predicted <MAT>
F:26-449/Product: #status predicted <SIG>
F:37-146/Domain: Clr/Cls repeat homology <CLR1>
F:159-270/Domain: Clr/Cls repeat homology <CLR2>
F:126/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:29_433/Binding site: carbohydrate (Asn) (covalent) #status predicted

RESULT 13
A:59271
Ra:reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
C:Accession: A59271
R:Thiel, S.; Vornur-Jensen, T.; Stover, C.M.; Schwaible, W.J.; Lauritsen, S.B.; Poulsen,
Nature 386, 506-510, 1997
A:Title: A second serine protease associated with mannan-binding lectin that activates
A:Reference number: A59271; MUID:97242412; PMID:9087411
A:Accession: A59271
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-686 <JEN>
A:Cross-references: GB:V09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627
A:Experimental source: tissue liver
A:Note: submitted to Genbank, December 1996
A:Note: parts of this sequence, including the amino end of the mature protein, were d
C:Genetics:
A:Gene: GDB:MASP2
A:Cross-references: GDB:6071500

for

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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 08:58:01 ; Search time 9 Seconds

(without alignments)
1589.926 Million cell updates/sec

Title: US-09-818-943-1

Sequence: 1 MSLFGLLVTSALAGQRGT.....DVALEHHECDVCRCSTG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179.5	9.7	928	NRPI_XENLA	P28824 xenopus lae
2	176	9.5	707	BMPL_XENLA	P98070 xenopus lae
3	173.5	9.3	616	SPAN_STRPU	P98068 strongyloce
4	169	9.1	986	BMPL_HUMAN	P13497 homo sapien
5	169	9.1	991	BMPL_MOUSE	P98065 mus musculu
6	164.5	8.9	931	NRP2_HUMAN	O60462 homo sapien
7	163.5	8.8	922	NRPI_RAT	O99499 rattus norv
8	163	8.8	925	NRP2_RAT	O35276 rattus norv
9	162.5	8.7	326	VEGD_RAT	O35251 rattus norv
10	160.5	8.6	923	NRPI_MOUSE	P97333 mus musculu
11	160.5	8.6	931	NRP2_MOUSE	O35375 mus musculu
12	159	8.5	1022	TLD_BRARE	O57460 brachydanio
13	158.5	8.5	923	NRPI_HUMAN	O14786 homo sapien
14	157	8.4	914	NRPI_CHICK	P79795 gallus gall
15	154	8.3	449	PCOL_HUMAN	Q15113 gallus gall
16	148.5	8.0	1057	TLD_DROME	P25723 drosophila
17	147	7.9	354	VEGD_HUMAN	O43815 homo sapien
18	143.5	7.7	686	MAS2_HUMAN	O00187 homo sapien
19	140	7.5	358	VEGD_MOUSE	P97946 mus musculu
20	139.5	7.5	597	BP10_PARLI	P42674 paracentrot
21	138.5	7.4	639	CRAR_MOUSE	P98064 mus musculu
22	138	7.4	705	BMPL_STRPU	P98065 strongyloce
23	138	7.4	699	CLR_HUMAN	P00736 homo sapien
24	137.5	7.4	699	CRAR_HUMAN	P48740 h complemen
25	132	7.1	419	VEGC_HUMAN	O49767 homo sapien
26	128	6.9	468	PCOL_MOUSE	O61398 mus musculu
27	128	6.9	468	PCOL_RAT	O08628 rattus norv
28	125	6.7	213	PDGA_RABIT	P34007 oryctolagus
29	125	6.7	415	VEGC_MOUSE	P97953 mus musculu
30	123.5	6.6	277	TS6G_HUMAN	P98066 homo sapien
31	120.5	6.5	245	PDGB_FELCA	P12919 felis silve
32	120.5	6.5	275	TS6G_MOUSE	O08859 mus musculu
33	118.5	6.4	276	TS6G_RABIT	P98065 oryctolagus

ALIGNMENTS

RESULT 1	ID	NRPI_XENLA	STANDARD:	PRT:	928 AA.
AC	P28824:				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Neuropilin-1 precursor (A5 protein) (A5 antigen).				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;				
OC	Xenopodidae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=91337458; PubMed=1908252;				
RA	Takegi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;				
RT	"The A5 antigen, a candidate for the neuronal recognition molecule,				
RL	has homologues to complement components and coagulation factors.";				
CC	Neuron 7:295-307(1991).				
CC	- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE				
CC	CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF				
CC	CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS				
CC	SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY				
CC	SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION				
CC	BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.				
CC	- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER				
CC	NEURONS.				
CC	- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.				
CC	- SIMILARITY: CONTAINS 2 CUB DOMAINS.				
CC	- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.				
CC	- SIMILARITY: CONTAINS 1 MAM DOMAIN.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: D10467; BAA01260.1; -				P52585 orf virus (
DR	HSSP: P12259; 1CZT				P01127 homo sapien
DR	InterPro: IPR000859; CUB_domain.				P13698 xenopus lae
DR	InterPro: IPR000421; FA5B_C.				P42664 xenopus lae
DR	InterPro: IPR000998; MAM_domain.				P28576 rattus norv
DR	Pfam: PF00431; CUB; 2.				P20033 mus musculu
DR	Pfam: PF00629; MAM; 1.				P20033 mus musculu
DR	Pfam: PF00754; F5_F8_type_C; 2.				P20033 mus musculu
DR	PRINTS: PRO0020; MAMDOMAIN.				P20033 mus musculu
DR	SMART: SM00042; CUB; 2.				P20033 mus musculu
DR	SMART: SM00231; FA5B_C; 2.				P20033 mus musculu
DR	SMART: SM00137; MAM; 1.				P20033 mus musculu
DR	PROSITE: PS00740; MAM_1; 1.				P20033 mus musculu

Query Match 9.3% Score 173.5; DB 1; Length 616;

	Best Local Similarity	27.0%, Pred. No. 2.8e-07,	Mismatches 70; Conservative 33; Mismatches 93; Indels 63; Gaps 14;
OY	56 GSISPRPHPTYPRTNTVLWRLVAEENWVLTQTFDEREGLEDPEDDICKYDFVEEPS	115	
Dd	349 GEITSPNPNSENVEDTACVEIEGPGSP-IELTF--LDMIEIETELICRYDAVEARKD	404	
OY	116 DGTILGRMGSGSYGVKGIISKGNQIRIFVSDETPPS--EPFGCHINYINVPQFLEANS	173	
Dd	405 INSIEKEKCGN-TLPVPVVISSSNMVMVFSTDS--PSTIRRGFKATYVILI-QTTIVEST	459	
OY	174 SVL--PPSALPLDLNNNAITAFSLIEDLIHYLEPERNQDLEDLYRPMWLGGKAFFVG	230	
Dd	460 TYLQTTPSTTLTQTNTNSTTLQT-----TNPSTTLTQTD--TPVIGSGGTEV-G	509	
OY	231 RKSRRVDNLTLTEEVRIYSCTPRNFVSIR-----ELKRPDYIF-----W	271	
Dd	510 VEGRASASNY-----PNDVDNSLQCCGYAEVDDGRVELLFEDFGLEDFTCNW	558	
OY	272 PGCLL-----VKRCG 201		
Dd	559 DSLMINLGCIKGMKMG 577		
 RESULT 4 BMP1_HUMAN STANDARD: PRT; 986 AA.			
ID	BMP1_HUMAN		
AC	P13497; Q13292; Q99421; Q99422; Q99423; Q14874; Q9UL38; Q13872;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)		
DN	(Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mtld).		
GN	BMP1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM BMP1-3).		
RC	TISSUE=Skin:		
RX	MEDLINE=96209868; PubMed=8643339;		
RA	Li S.W., Stetler A.L., Fertala A., Hojima Y., Arnold W.V.,		
RT	Procokop D.J.;		
RT	"The C-proteinase that processes procollagens to fibrillar collagens		
RT	is identical to the protein previously identified as bone morphogenic		
RT	protein-1.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM BMP1-1).		
RX	MEDLINE=89072730; PubMed=3201241;		
RA	Mooney J.M., Rosen V., Celeste A.J., Mitsos L.M., Whitters M.J.,		
RA	Kitz R.W., Hewick R.M., Wang E.A.;		
RT	"Novel regulators of bone formation: molecular clones and		
RT	activities.";		
RL	Science 242:1528-1534(1988).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).		
RC	TISSUE=Placenta:		
RX	MEDLINE=96160316; PubMed=9500680;		
RA	Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;		
RT	"Three alternatively spliced variants of the gene coding for the human		
RT	bone morphogenetic protein-1.";		
RL	J. Mol. Med. 76:141-146(1998).		
RN	[4]		
RP	PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).		
RC	TISSUE=Placenta:		
RX	MEDLINE=95096114; PubMed=7798260;		
RA	Takahara K., Lyons G.E., Greenspan D.S.;		
RT	"Bone morphogenetic protein-1 and a mammalian tolloid homologue (mtld)		
RT	are encoded by alternatively spliced transcripts which are		
RT	differentially expressed in some tissues.";		
RL	J. Biol. Chem. 269:32572-32578(1994).		

RC STRAIN=C57BL/6; TISSUE=Embryo;
RA MEDLINE-94229342; PubMed-8174772;
RX Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
RT "Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
RT which is related to the Drosophila dorsventral gene tollid and
RT encodes a putative astacin metalloendopeptidase.";
RL Dev. Biol. 163:175-183(1994).
CC -1- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II
CC AND II. INDUCES CARTILAGE AND BONE FORMATION.
CC -1- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC Ala-1-asp in type I and II procollagens and at Arg-1-asp in type
CC III.
CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC -1- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-
CC ENDOPEPTIDASE ENHANCER PROTEIN.
CC -1- TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC MATERIAL, DECIDUUM
CC AND FLOOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING
CC MEMBRANOUS AND ENDOCHONDRAL BONE, SUBMUCOSA OF INTESTINE, DERMIS
CC OF SKIN AND THE MESENCHYME OF SPLEEN AND LUNG.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 5 CUB DOMAINS.

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CC EMBL: L24755; AAA37306.1; -
CC DR HSSP: P00736; IAP0.
CC DR MEROPS: M12.005; -
CC DR MGD: MGI:88176; Bmp1.
CC DR InterPro: IPR001506; Astacin.
CC DR InterPro: IPR000152; Asx_hydroxyl.
CC DR InterPro: IPR000859; CUB_domain.
CC DR InterPro: IPR000561; EGF-like.
CC DR InterPro: IPR001881; EGF_Ca.
CC DR InterPro: IPR000130; Zn_Mrpeptidse.
CC DR Pfam: PF00008; EGF_2.
CC DR Pfam: PF00431; CUB_5.
CC DR Pfam: PF01400; Astacin_1.
CC DR PRINTS: PRO0480; ASTACIN.
CC DR SMART: SM00042; CUB_5.
CC DR SMART: SM00179; EGF_CA; 2.
CC DR SMART: SM00235; ZNMG; 1.
CC DR PROSITE: PS00142; ZINC_PROTEASE; 1.
CC DR PROSITE: PS01180; CUB_5.
CC DR PROSITE: PS00010; ASX_HYDROXYL; 2.
CC DR PROSITE: PS00022; EGF_1; FALSE_NEG.
CC DR PROSITE: PS01186; EGF_2; 2.
CC DR PROSITE: PS01187; EGF_CA; 2.
CC DR Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase;
CC Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
CC Glycoprotein; Zymogen.
CC KW SIGNAL: 1 25 POTENTIAL.
CC FT PROPEP 26 125 POTENTIAL.
CC FT CHAIN 126 991 BONE MORPHOGENETIC PROTEIN 1.
CC FT DOMAIN 126 326 METALLOPROTEASE.
CC FT DOMAIN 327 439 CUB 1.
CC FT DOMAIN 440 551 CUB 2.
CC FT DOMAIN 552 593 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
CC FT DOMAIN 596 707 CUB 3.
CC FT DOMAIN 708 748 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
CC FT DOMAIN 752 864 CUB 4.
CC FT DOMAIN 865 981 CUB 5.
CC FT METL 218 218 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT ACT_SITE 219 219 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT METL 222 222 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT METL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT DISULFID 327 353 BY SIMILARITY.

FT DISULFID 380 402 BY SIMILARITY.
FT DISULFID 440 466 BY SIMILARITY.
FT DISULFID 493 515 BY SIMILARITY.
FT DISULFID 556 568 BY SIMILARITY.
FT DISULFID 564 577 BY SIMILARITY.
FT DISULFID 579 592 BY SIMILARITY.
FT DISULFID 596 622 BY SIMILARITY.
FT DISULFID 649 671 BY SIMILARITY.
FT DISULFID 712 723 BY SIMILARITY.
FT DISULFID 719 732 BY SIMILARITY.
FT DISULFID 734 747 BY SIMILARITY.
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 604 604 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 991 AA; 111607 MW; 68A1847783A0BB9E CRC64;
Query Match 9.1%; Score 169; DB 1; Length 991;
Best local Similarity 39.4%; Pred. No. 1.3e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;
QY 55 NSGHSHPREPHYPRNTVLVRLVA-VEENWVQLPDERFERGLEDEDDICKRYDVEVEE 113
Db 604 NSGHSHPREPHYPRNTVLVRLVA-VEENWVQLPDERFERGLEDEDDICKRYDVEVEE 113
QY 114 --PSDGTILGRMGSGTVPKQSKNGNIRIRVSDYFSEFGCLHY 160
Db 659 GLTADSKLHGKFGCS-EKPEVITSQYNNMVFERSDNTV-SKKGFAHF 705
RESULT 6
NRP2_HUMAN
ID NRP2_HUMAN STANDARD: PRT: 931 AA.
AC 060462; O14820; O14821;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
DE receptor 2).
GN NRP2 OR VEGF165R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
RX MEDLINE-97470888; PubMed-9331348;
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
RT "Neuropilin-2, a novel member of the neuropilin family, is a high
RT affinity receptor for the semaphorins Sema F and Sema IV but not Sema
RT III.";
RL Neuron 19:547-559(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A22).
RC TISSUE=Breast;
RX MEDLINE-98188099; PubMed-9529250;
RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;
RT "Neuropilin-1 is expressed by endothelial and tumor cells as an
RT isoform-specific receptor for vascular endothelial growth factor.";
RL Cell 92:735-745(1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE-20309748; PubMed-10748121;
RA Guzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid
RT form of vascular endothelial growth factor (VEGF) and of placenta
RT growth factor-2, but only neuropilin-2 functions as a receptor for
RT the 145-amino acid form of VEGF.";
RL J. Biol. Chem. 275:18040-18045(2000).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC -1- SUBUNIT: NEUROFILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH

```

CC NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms: A22 (SHOWN HERE), A0 AND A17;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC
CC EMBL: AF022859; AAC51788.1; -.
CC EMBL: AF022860; AAC51789.1; -.
CC EMBL: AF016098; AAC12922.1; -.
CC HSSP: P12259; ICZT.
CC Genew: HGNC:8005; NRP2.
CC MIM: 602070; -.
CC InterPro: IPR000859; CUB_domain.
CC InterPro: IPR000421; FA58_C.
CC InterPro: IPR000998; MAM_domain.
CC Pfam: PF00431; CUB; 2.
CC Pfam: PF00629; MAM; 1.
CC Pfam: PF00754; F5_F8_type_C; 2.
CC SMART: SM00042; CUB; 2.
CC SMART: SM00231; FA58C; 2.
CC SMART: SM00137; MAM; 1.
CC PROSITE: PS01180; CUB; 2.
CC PROSITE: PS01285; FA58C_1; 2.
CC PROSITE: PS01286; FA58C_2; 2.
CC PROSITE: PS50060; MAM_2; 1.
CC Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
KW Alternative splicing.
KW
KW SIGNAL 1 20 OR 22 (POTENTIAL).
KW CHAIN 21 931 NEUROPILIN-2.
KW DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).
KW TRANSMEM 865 889 POTENTIAL.
KW DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).
KW DOMAIN 28 142 CUB 1.
KW DOMAIN 149 267 CUB 2.
KW DOMAIN 277 427 F5/8 TYPE C 1.
KW DOMAIN 434 592 F5/8 TYPE C 2.
KW DOMAIN 642 802 MAM.
KW DOMAIN 671 674 POLY-SER.
KW DOMAIN 28 35 BY SIMILARITY.
KW DISULFID 83 105 BY SIMILARITY.
KW DISULFID 149 175 BY SIMILARITY.
KW DISULFID 208 230 BY SIMILARITY.
KW DISULFID 277 427 BY SIMILARITY.
KW DISULFID 434 592 BY SIMILARITY.
KW CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW CARBOHYD 839 839 N-LINKED (GLCNAC. . .) (POTENTIAL).
KW VARSPALIC 809 813 MISSING (IN ISOFORM A17).
KW VARSPALIC 809 830 MISSING (IN ISOFORM A0).
KW CONFLICT 602 602 E -> K (IN REF. 1).
SQ SEQUENCE 931 AA: 104830 MW: 270CBAB69A0A797C CRC64:

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Query Match 8.9%; Score 164.5; DB 1; Length 931;
 Best Local Similarity 29.9%; Pred. No. 2.8e-06;
 Matches 49; Conservative 20; Mismatches 70; Indels 25; Gaps 5;

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QY 1 MSFGLLVTSAGORRGTQAESNLSSKRFSSKQNGVDPQHRITVTSNGSIHS 60
  | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MDMPPLTWLWVLA-----YSRHYVRQPPPPCGRLNSKDAGITTS 42

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QY 61 PRPPTPTNTVTLWRLVAEENWVQLTFDERFGLEDPEDICKYDFEVE--EPDGT 118

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Db 43 PGYQDPYSHONCEMIYVAPENOKIYLVNFPHEIEKHD---CKYPIEIRDSDSAD 99
  | : | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 119 ILGWCQSGYTPGQOISNGNOIRIRFVSDEFPSPSPCHRYNI 162
  | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 100 ILGRHCGN-IAPPTLISSGSMYTKFTSD-YARQAGFSLEYEI 141

RESULT 7
NRPL_RAT NRPL_RAT STANDARD; PRT; 922 AA.
AC Q9QWU9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
DE receptor).
GN NRPL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.;
RT "Neuropilin is a semaphorin III receptor.";
RL Cell 90:753-762(1997).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOMERIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: FOUND IN THE EMBRYONIC NERVOUS SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC
CC EMBL: AF016296; AAC53337.1; -.
CC HSSP: P12259; ICZT.
CC InterPro: IPR000859; CUB_domain.
CC InterPro: IPR000421; FA58_C.
CC InterPro: IPR001092; HLH_basic.
CC InterPro: IPR000998; MAM_domain.
CC Pfam: PF00431; CUB; 2.
CC Pfam: PF00629; MAM; 1.
CC Pfam: PF00754; F5_F8_type_C; 2.
CC PRINTS: PR00020; MAMDOMAIN.
CC SMART: SM00042; CUB; 2.
CC SMART: SM00231; FA58C; 2.
CC SMART: SM00137; MAM; 1.
CC PROSITE: PS01180; CUB; 2.
CC PROSITE: PS01285; FA58C_1; 2.
CC PROSITE: PS01286; FA58C_2; 2.
CC PROSITE: PS00740; MAM_1; 1.
CC PROSITE: PS00600; MAM_2; 1.
KW Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.
KW SIGNAL 1 21 POTENTIAL.

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FT CHAIN 22 922 NEUROFILIN-1.
FT DOMAIN 22 855 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 856 880 POTENTIAL.
FT DOMAIN 881 922 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 583 F5/8 TYPE C 2.
FT DOMAIN 645 811 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 BY SIMILARITY.
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 841 841 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 922 AA; 103082 MW; CC6F82AD098B0F2E CRC64;

Query Match 8.8%; Score 163.5; DB 1; Length 922;
Best Local Similarity 36.5%; Pred. No. 3.4e-06;
Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;

QY 50 ITVSTNGSIHSPRPHTYRNTVLVRLVAEENWVLIOLTPFEREGLEDPEDDICKYDFV 109
DB 31 IRIENBGYITSPGYSPHSPSEKCEWLIOAPEYORIMNFNHFLEPRD---CKYDYV 87

QY 110 EV-EEPSDGTILGRCWGSCTVPGKQISKGNQIRIRFVSDEYFPSPGCIHYNI 162
DB 88 EVIDENEGGRLMKCKCKR-IAPSPVSSGPFILIKFVSD-YETHAGGSIREI 140

RESULT 8
NR2_RAT STANDARD; PRT; 925 AA.
ID NR2_RAT 035276;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Neutrophilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
GN NR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=97433085; Pubmed=9288754;
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.;
RT "Neutrophilin is a semaphorin III receptor.";
RL Cell 90:753-762(1997).

CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
CC AND VEGF-145 ISOMERS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE
CC CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE
CC LINING IN THE RIBS.
CC -1- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC -----
DB EMBL: AF016297; AAC53338.1; -.
DR HSP; P12259; IC2T.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00629; MAM; 1.
DR Pfam: PF00754; F5_F8_Type_C; 2.
DR SMART: SM00042; CUB; 2.
DR SMART: SM00231; FA58C; 2.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS01285; FA58C_1; 2.
DR PROSITE: PS01286; FA58C_2; 2.
DR PROSITE: PS50060; MAM_2; 1.
KW Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
FT SIGNAL 1 22
FT CHAIN 23 925
FT DOMAIN 23 858 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 859 883 POTENTIAL.
FT DOMAIN 884 925 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 142 CUB 1.
FT DOMAIN 149 267 CUB 2.
FT DOMAIN 277 427 F5/8 TYPE C 1.
FT DOMAIN 434 592 F5/8 TYPE C 2.
FT DOMAIN 642 802 MAM.
FT DISULFID 28 55 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 833 833 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 925 AA; 103896 MW; 3BF62903F644851C CRC64;

Query Match 8.8%; Score 163; DB 1; Length 925;
Best Local Similarity 33.8%; Pred. No. 3.8e-06;
Matches 45; Conservative 20; Mismatches 60; Indels 8; Gaps 5;

QY 32 FSSNKQNGVQDPQHERITVTSTNGSIHSPRPHTYRNTVLVRLVAEENWVLIQTFD 91
DB 15 FSGHKVRS-QDPPCGGRINSKDGAYITSPGYFDYSHQNCENWVYADEPNQIVLNFN 73

QY 92 ERFGLEDPPEDDICKYDFVE--EPDGTILGRCWGSCTVPGKQISKGNQIRIRFVSDEY 149
DB 74 PHEIEKHD---CKYDFEIRDDSDADLLGKHGCGN-IAPPTISSGSVLVIKFTSD-Y 128

QY 150 FPSEPGCIHYNI 162
DB 129 ARQAGFSLRYEL 141

RESULT 9
VEGD_RAT STANDARD; PRT; 326 AA.
ID VEGD_RAT 035251;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).
GN FIGF OR VEGFD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RA Yamada Y., Hirata Y., Nezu J., Shimane M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC and endothelial cell growth, stimulating their proliferation and
CC migration and also has effects on the permeability of blood
CC vessels. May function in the formation of the venous and lymphatic
CC vascular systems during embryogenesis, and also in the maintenance
CC of differentiated lymphatic endothelium in adults. Binds and
CC activates VEGFR-3 (Flt4) receptor (By similarity).
CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- PTM: Undergoes a complex proteolytic maturation which generates a
CC variety of processed secreted forms with increased activity toward
CC VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC linked by disulfide bonds before secretion. The fully processed
CC VEGF-D is composed mostly of two VEGF homology domains (VHDS)
CC bound by non-covalent interactions (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF014827; AAB66557.1; -
CC DR HSSP: P15692; IVP.
CC DR InterPro: IPR004153; CXXC.repeat.
CC DR InterPro: IPR000072; PD_growth_factor.
CC DR Pfam: PF00341; PDGF; 1.
CC DR Pfam: PF03128; CXXC; 1.
CC DR ProDom: PD001629; PD_growth_factor; 1.
CC DR SMART: SM00141; PDGF; 1.
CC DR PROSITE: PS00249; PDGF_1; 1.
CC DR PROSITE: PS50278; PDGF_2; 1.
CC DR Mitogen: Growth factor; Glycoprotein; Signal; Repeat;
CC Cleavage on pair of basic residues; Multigene family.
CC KW SIGNAL.
CC FT PROPEP 1 21
CC FT CHAIN 94 210
CC FT PROPEP 211 326
CC FT DOMAIN 227 317
CC FT REPEAT 227 242
CC FT REPEAT 263 278
CC FT REPEAT 282 298
CC FT REPEAT 306 317
CC FT DISULFID 116 158
CC FT DISULFID 147 194
CC FT DISULFID 151 196
CC FT DISULFID 141 141
CC FT DISULFID 150 150
CC FT CARBOHYD 160 160
CC FT CARBOHYD 190 190
CC FT CARBOHYD 292 292
CC SQ SEQUENCE 326 AA; 37112 MW; 1261AFA373596C00 CRC64;

Query Match 8.7%; Score 162.5; DB 1; Length 326;
Best Local Similarity 30.0%; Pred. No. 1,1e-06;
Matches 61; Conservative 23; Mismatches 80; Indels 39; Gaps 9;

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QY 263 L-KRTDIFMPGCLLYKRCGNCACCLHNCNECOY---PSKVTKKYHVLQLRPKTVGR 318
DB 129 LKGTITTFRRPCVNVNFRCG---CC--NEESYMCANTSTSYISKLFELISV--PLTSV- 180
QY 319 GLHKSLLTDALEHNEHCDCVCRG 341
DB 181 ---PELVVPIANHNHCCKLPTG 200

RESULT 10
ID NRPI_MOUSE STANDARD; PRT; 923 AA.
AC P97333;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neupilin-1 precursor (A5 protein).
GN NRPI OR NRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c; TISSUE-Embryonic brain;
RX MEDLINE=96353149; PubMed=8748368;
RA Kawakami A., Kitsuikawa T., Takagi S., Fujisawa H.;
RT Developmentally regulated expression of a cell surface protein,
RT neupilin, in the mouse nervous system";
RL J. Neurobiol. 29:1-17(1996).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS, AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF KDR, THE VEGF-165
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D50086; BAA08789.1; -
CC DR HSSP: P12259; IC2T.
CC DR MGD: MGI:106206; Nrp.
CC DR InterPro: IPR000859; CUB_domain.
CC DR InterPro: IPR000421; FA58_C.
CC DR InterPro: IPR000998; MAM_domain.
CC DR Pfam: PF00431; CUB; 2.
CC DR Pfam: PF00629; MAM; 1.
CC DR Pfam: PF00754; F5_F8_Type_C; 2.
CC DR SMART: SM00042; CUB; 2.
CC DR SMART: SM00231; FA58C; 2.
CC DR SMART: SM00137; MAM; 1.
CC DR PROSITE: PS01180; CUB; 2.
CC DR PROSITE: PS01285; FA58C_1; 2.
CC DR PROSITE: PS01286; FA58C_2; 2.
CC DR PROSITE: PS00740; MAM_1; 1.
CC DR PROSITE: PS00660; MAM_2; 1.
CC DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.
FT SIGNAL 1 21

```

```
CC -I- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -I- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -I- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
```

FI	CONFLICT	786	786	G
SQ	SEQUENCE	931 AA;	104558 MW;	

8.68; Score 160.5; DB 1; Length 931;

Best Local Similarity 30.5%; Pred. No. 6,3e-06;
Matches 50; Conservative 18; Mismatches 71; Indels 25; Gaps 5;

OY 1 MSFGLLYTALAGORGAESNLSSKFOFSKQNGVOPQHRRITTVNGSIHS 60
Db 1 MDMPPLTWLWAL-----YFSGHEVRSQODPPCGRPNKADGVITS 42
OY 61 PRPPHTYPRNTVWRLVAEENWIDTFDERFGLDPDDICKYDFEVE--EPEDGF 118
Db 43 PGYPODYPSNONGEMVIYAEPNOKIYLNPNPHEIFKHDP---CKYDFIIRGDSDESAD 99
OY 119 IIGRWCGSGTVPGKQISKGNQIRIYVSDYFSPSEPGFCIHYNI 162
Db 100 LIGKHCN-IAPPTIISGSLVYIKFTSD-YARGAGFSLRYEL 141

RESULT 12
TLD_BRAVE STANDARD; PRT; 1022 AA.

AC 057460;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dorsal-ventral patterning tolloid protein precursor (EC 3.4.24.-)
DE (Mini fin protein).
GN TOLLOID OR TLD OR MFN.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RE SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE-gastrula;
RA MEDLINE=98057457; PubMed=9395394;
RA Blader P., Kastegar S., Fischer N., Straehle U.;
RT "Cleavage of the BMP-4 antagonist chordin by zebrafish tolloid.";
RL Science 278:1937-1940(1997).
RN [2]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=99307076; PubMed=10375503;
RA Connors S.A., Trout J., Ekker M., Mullins M.C.;
RT "The role of tolloid/mini fin in dorsoventral pattern formation of the
RT zebrafish embryo.";
RL Development 126:3119-3130(1999).
CC -1- FUNCTION: Required for patterning ventral tissues of the tail. May
CC increase bone morphogenetic protein (BMP) activity at the end of
CC gastrulation by proteolytic cleavage of chordin and release of BMP
CC from inactive complexes.
CC -1- TISSUE SPECIFICITY: During gastrulation, accumulates around the
CC closing blastopore with greater expression ventrally. At the
CC animal pole, expressed in the ectoderm flanking the anterior
CC neural plate. At the 10-somite stage, expressed in the developing
CC tailbud and cranial neural crest. At the 20-somite stage, also
CC expressed in the hematopoietic system.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 5 CUB DOMAINS.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF027596; AAC60304.1; -
CC DR HSSP: P35555; 1EMN.
DR HEROS: M12.016; -
DR ZFIN: ZDB-GENE-990415-265; tolloid.
DR InterPro: IPR001506; Astacin.
DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000130; Zn_TFPeptidase.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00431; CUB; 5.
DR Pfam: PF01400; Astacin; 1.
DR PRINTS: PR00480; ASTACIN..
DR SMART: SM00042; CUB; 5.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00179; EGF_CA; 2.
DR SMART: SM00235; ZmC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 2.
DR PROSITE: PS01180; CUB; 5.
DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR Developmental protein; Hydrolase; Protease; Metalloprotease; Zinc;
KW Metal-binding; Calcium; EGF-like domain; Repeat; Signal; Glycoprotein;
KW Zymogen.
KW SIGNAL. 1 32
FT PROPEP 33 156
FT CHAIN 157 1022
FT DOMAIN 157 1022
FT METAL 896 1012
FT ACT_SITE 249 249
FT METAL 250 250
FT METAL 253 253
FT METAL 259 259
FT DISULFID 358 384
FT DISULFID 411 433
FT DISULFID 471 497
FT DISULFID 524 546
FT DISULFID 587 599
FT DISULFID 595 608
FT DISULFID 610 623
FT DISULFID 627 633
FT DISULFID 680 702
FT DISULFID 743 754
FT DISULFID 750 763
FT DISULFID 765 778
FT DISULFID 783 809
FT DISULFID 836 858
FT DISULFID 896 926
FT DISULFID 953 975
FT CARBOHYD 129 129
FT CARBOHYD 178 178
FT CARBOHYD 368 368
FT CARBOHYD 399 399
FT CARBOHYD 635 635
SQ SEQUENCE 1022 AA; 115536 MW; A68CA1D0E4173F9 CRC64;

Query Match 8.6%; Score 159; DB 1; Length 1022;
Best Local Similarity 39.8%; Pred. No. 9,6e-06;
Matches 43; Conservative 19; Mismatches 38; Indels 8; Gaps 6;

OY 55 NGSISPRPHTYPRNTVWRLVAEENWIDTFDERFGLDPDDICKYDFEVEE- 113
Db 635 NGITTPGPKXEYPRKNCWQVAVPQ-YRISMQF-EAELEGG--NECKYIVVEVRSG 690
OY 114 -PSDGTILGRWCGSGTVPGKQISKGNQIRIYVSDYFSPSEPGFCIHY 160
Db 691 LSSDSKIHGKYCGT-EVPEVITSQYNNMRIEFSKSDMTV-SKQGFKAHF 736

RESULT 13
NRPL_HUMAN STANDARD; PRT; 923 AA.
AC 014786; 060461.
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neupilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).
GN NRPL OR NRP OR VEGF165R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM).
RX MEDLINE=97433084; PubMed=9288753;
RA He Z., Tessier-Lavigne M.;
RT "Neupilin is a receptor for the axonal chemorepellent semaphorin III."
RL Cell 90:739-751(1997).
RN [2]
RP SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM), AND SEQUENCE OF 22-39.
RX TISSUE=Breast;
MEDLINE=98188099; PubMed=9529250;
RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;
RT "Neupilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."
RL Cell 92:735-745(1998).
RN [3]
RP SEQUENCE FROM N.A. (SOLUBLE/SNRP1 ISOFORM), AND SEQUENCE OF 22-31.
RX TISSUE=Prostatic adenocarcinoma;
MEDLINE=20183929; PubMed=1068880;
RA Gagnon M.L., Bieleberg D.R., Gechtman Z., Miao H.-Q., Takashima S., Soker S., Klagsbrun M.;
RT "Identification of a natural soluble neupilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor activity."
RL Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=20309748; PubMed=10748121;
RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
RT "Neupilin-2 and neupilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neupilin-2 functions as a receptor for the 145-amino acid form of VEGF."
RL J. Biol. Chem. 275:18040-18045(2000).
CC -1- FUNCTION: THE MEMBRANE-BOUND ISOFORM IS A RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B.
CC COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS.
CC -1- FUNCTION: THE SOLUBLE/SNRP1 ISOFORM BINDS VEGF-165 AND APPEARS TO INHIBIT ITS BINDING TO CELLS. IT MAY ALSO INDUCE APOPTOSIS BY SEQUESTERING VEGF-165. MAY BIND AS WELL VARIOUS MEMBERS OF THE SEMAPHORIN FAMILY. ITS EXPRESSION HAS AN AVERSE EFFECT ON BLOOD VESSEL NUMBER AND INTEGRITY.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SOLUBLE/SNRP1 ISOFORM IS SECRETED.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, MEMBRANE-BOUND (SHOWN HERE) AND SOLUBLE/SNRP1 ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: THE EXPRESSION OF MEMBRANE-BOUND AND SOLUBLE/SNRP1 ISOFORMS DOES NOT SEEM TO OVERLAP. THE MEMBRANE-BOUND ISOFORM IS EXPRESSED BY THE BLOOD VESSELS OF DIFFERENT TISSUES. IN THE DEVELOPING EMBRYO IT IS FOUND PREDOMINANTLY IN THE NERVOUS SYSTEM. IN ADULT TISSUES, IT IS HIGHLY EXPRESSED IN HEART

CC AND PLACENTA; MODERATELY IN LUNG, LIVER, SKELETAL MUSCLE, KIDNEY
CC AND PANCREAS; AND LOW IN ADULT BRAIN. THE SOLUBLE/SNRP1 ISOFORM IS
CC FOUND IN LIVER HEPATOCYTES, KIDNEY DISTAL AND PROXIMAL TUBULES.
CC -1- SIMILARITY: BELONGS TO THE NEUPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF018956; AAC51759.1; -
CC EMBL: AF016050; AAC12921.1; -
CC EMBL: AF145712; AAF4344.1; -
CC HSSP; P12259; 1CZF.
CC GeneW; HGNC:8004; NRPL.
CC MIM; 602069; -
CC InterPro: IPR000859; CUB_domain.
CC InterPro: IPR000421; FASB_C.
CC InterPro: IPR001092; HLH_basic.
CC InterPro: IPR000998; MAM_domain.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00629; MAM; 1.
CC Pfam; PF00754; F5_F8_type_C; 2.
CC PRINTS; PRO0020; MAMDOMAIN.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00231; FASB_C; 2.
CC SMART; SM00137; MAM; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01285; FASB_C; 1; 2.
CC PROSITE; PS01286; FASB_C; 2; 2.
CC PROSITE; PS00740; MAM; 1; 1.
CC PROSITE; PS50060; MAM; 2; 1.
CC Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
CC Alternative splicing.
CC FT SIGNAL 1 21
FT CHAIN 22 923 NEUPILIN-1.
FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 857 879 POTENTIAL.
FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 583 F5/8 TYPE C 2.
FT DOMAIN 645 811 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 424 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 842 842 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 642 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 'VARSPPLIC 645 923 EFP -> GIK (IN SOLUBLE/SNRP1 ISOFORM).
FT CONFLICT 26 26 MISSING (IN SOLUBLE/SNRP1 ISOFORM).
FT CONFLICT 749 749 K -> E (IN REF. 1).
FT CONFLICT 749 749 D -> H (IN REF. 2).
FT CONFLICT 855 855 E -> D (IN REF. 2).
SQ SEQUENCE 923 AA; 103120 MW; ADEADCA4A9B5D57 CRC64;
Query Match 8.5%; Score 158.5; DB 1; Length 923;
Best Local Similarity 35.7%; Pred. No. 9,3e-06;
Matches 41; Conservative 18; Mismatches 49; Indels 7; Gaps 4;
OY 50 ITVSTGSHSPRPHPTHTYVRLVLAEEVNWILTFDERFGLDEPEDDICKYDFV 109

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Db      31 IKIESPGYLSPGYPHSPSEKCEMLIQAPDPYORIMINFNPHFLEDRD---CKDYV 87
QY      110 EV--EERSDGTILGRMGSGTVPKQISKGNQIRVSPSEFSEFGFCHINYI 162
Db      88 EVDGENENGFHFGKFCGK-IAPPVVSQGFLEIKFVSD-YETHGAGFSIRVEI 140

RESULT 14
NRPL_CHICK STANDARD: PRT; 914 AA.
ID NRPL_CHICK
AC P/9795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropilin-1 precursor (A5 protein).
GN NRPL OR NRP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Embryonic brain;
RX MEDLINE=95324761; PubMed=7601310;
RA Takagi S., Kasuya Y., Shimizu M., Matsura T., Tsuboi M., Kawakami A.,
RA Fujisawa H.;
RT "Expression of a cell adhesion molecule, neuropilin, in the
RT developing chick nervous system.";
RQ Dev. Biol. 170:207-222(1995).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOKINE ACTIVITY OF SEMAPHORINS (BY
CC SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
CC PROPERTIES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM
CC (LAYERS D AND E OF GSEs); AMACRINE CELLS OF RETINA; NEURITES OF
CC DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, E.G.
CC BLOOD VESSELS IN THE ENTIRE EMBRYO.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; DA5416; BAA08256.1; -
CC HSSP; P12259; ICZT.
CC InterPro: IPR000859; CUB domain.
CC InterPro: IPR000421; FA58_C.
CC InterPro: IPR000936; MAM_domain.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00754; F5_F8_type_C; 2.
CC PRINTS; PR00020; MAMDOMAIN.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00231; FA58C; 2.
CC SMART; SM00137; MAM; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01285; FA58C_1; 2.
CC PROSITE; PS01286; FA58C_2; 2.
CC PROSITE; PS00740; MAM_1; 1.
CC PROSITE; PS00650; MAM_2; 1.
CC Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
KW

```

```

KW      Cell adhesion.
FT SIGNAL 1 18
FT CHAIN 19 914
FT DOMAIN 20 847
FT TRANSMEM 848 870
FT DOMAIN 871 914
FT DOMAIN 25 139
FT DOMAIN 145 263
FT DOMAIN 273 422
FT DOMAIN 429 581
FT DOMAIN 636 801
FT DISULFID 25 52
FT DISULFID 80 102
FT DISULFID 145 171
FT DISULFID 204 226
FT DISULFID 273 422
FT DISULFID 429 581
SQ SEQUENCE 914 AA; 102480 MW; DD2EED6F0CBB68C CRC64;

Query Match 8.4%; Score 157; DB 1; Length 914;
Best Local Similarity 29.4%; Pred. No. 1.2e-05;
Matches 52; Conservative 27; Mismatches 68; Indels 30; Gaps 9;

QY      50 ITVSTNGSIHSPREPTYPNTVLAWEVLEENWVQLTFDERFGLDEPDICKYFV 109
Db      29 IKILSPGYLSPGYPHSPSEKCEMLIQAPDPYORIMINFNPHFLEDRD---CKDYV 85
QY      110 EV--EERSDGTILGRMGSGTVPKQISKGNQIRVSPSEFSEFGFCHINYI--P 165
Db      86 EVIDGDNAEGRMGKFCGK-IAPPVVSQGFLEIKFVSD-YETHGAGFSIRVEKRG 143
QY      166 Q---FTEAVSPSVLP--PSALPLDL-----LNMTFTFTLEDIRYLEPE 206
Db      144 ECSRNFSSSGMFKSPFPFKYNSLECTYITAPKMSILLFESE-----LEPD 195

RESULT 15
PCOL_HUMAN STANDARD: PRT; 449 AA.
ID PCOL_HUMAN
AC 015113; O14550;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I
DE procollagen COOH-terminal proteinase enhancer) (Type I procollagen C-
DE DE proteinase enhancer protein).
GN PCOLCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95014462; PubMed=7523404;
RA Takahara K., Kessler E., Blinamnov L., Brusel M., Eddy R.L.,
RA Jani-Sait S., Shows T.B., Greenspan D.S.;
RT "Type I procollagen COOH-terminal proteinase enhancer protein:
RT identification, primary structure, and chromosomal localization of the
RT cognate human gene (PCOLCE).";
RT J. Biol. Chem. 269:26280-26285(1994).
RN [2]
RP REVISIONS TO 56; 154 AND 373.
RA Kessler E.;
RL Unpublished observations (FEB-2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Hirahara I., Syoutuda K., Harada K., Tomita M., Urakami K., Terai H.,
RA Morisaki N., Saito Y.;
RT "Smooth muscle cell derived procollagen C-protease enhancer protein.";
RL Cell Struct. Funct. 21:662-662(1996).
RN [4]

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Db 301 VTKKYEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNMAG 345

RESULT 2

US-09-040-220D-2
Sequence 2, Application US/09040220D

Patent No. 6391311

GENERAL INFORMATION:

APPLICANT: Ferrara, Napoleone

APPLICANT: Kuo, Sophia S.

TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR

TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC

TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,

FILE REFERENCE: P1122

CURRENT APPLICATION NUMBER: US/09/040,220D

CURRENT FILING DATE: 1998-03-17

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 2

LENGTH: 345

TYPE: PRT

ORGANISM: Human

US-09-040-220D-2

Query Match 90.2%; Score 1667; DB 4; Length 345;

Best Local Similarity 87.0%; Pred. No. 4,6e-175;

Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Db 1 MLLGLLLTSALAGQGTGTRAESNLSKQLQSDKEQNGVQDPRHRRVYVITSGNSIHS 60

Db 1 MSFGLLLTSALAGQGTGTRAESNLSKQFQSSNKEQNGVQDPRHRRVYVITSGNSIHS 60

QY 61 PKPHTYPRNMVLYWRVAVDENVRIQITFDERGLEDPEDDICKYDFVEVEEPPSDGTYL 120

Db 61 PREPHTYPRNTVLYWRVAVDENVRIQITFDERGLEDPEDDICKYDFVEVEEPPSDGTYL 120

QY 121 GRMGSGTVPGKQTSKGNHRIREFVSDYEPSEPGFCIHNIIMPQVTEYTSVLPSS 180

Db 121 GRMGSGTVPGKQTSKGNHRIREFVSDYEPSEPGFCIHNIIMPQVTEYTSVLPSS 180

QY 181 LSIDLNNATAPSTLELIRYLEPRDQWYDLSLYKPTMOLGKAFYGRKSKVYVNL 240

Db 181 LPDLNNATAPSTLELIRYLEPRDQWYDLSLYKPTMOLGKAFYGRKSKVYVNL 240

QY 241 LKEEVKLYSCTPRNFYSIREELKRTDTIFWPGCLVYKRCGNACCLHNCNEQCVPRK 300

Db 241 LKEEVKLYSCTPRNFYSIREELKRTDTIFWPGCLVYKRCGNACCLHNCNEQCVPRK 300

QY 301 VTKKYEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNMAG 345

Db 301 VTKKYEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNMAG 345

RESULT 3

US-09-457-066-2

Sequence 2, Application US/09457066

Patent No. 6432673

GENERAL INFORMATION:

APPLICANT: Gao, Zeren

APPLICANT: Hart, Charles E.

APPLICANT: Piddington, Christopher S.

APPLICANT: Sheppard, Paul O.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF3

FILE REFERENCE: 98-60

CURRENT APPLICATION NUMBER: US/09/457,066

CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 345

TYPE: PRT
ORGANISM: Homo sapiens
US-09-457-066-2

Query Match 90.2%; Score 1667; DB 4; Length 345;

Best Local Similarity 87.0%; Pred. No. 4,6e-175;

Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGQGTGTRAESNLSKQLQSDKEQNGVQDPRHRRVYVITSGNSIHS 60

Db 1 MSFGLLLTSALAGQGTGTRAESNLSKQFQSSNKEQNGVQDPRHRRVYVITSGNSIHS 60

QY 61 PKPHTYPRNMVLYWRVAVDENVRIQITFDERGLEDPEDDICKYDFVEVEEPPSDGTYL 120

Db 61 PREPHTYPRNTVLYWRVAVDENVRIQITFDERGLEDPEDDICKYDFVEVEEPPSDGTYL 120

QY 121 GRMGSGTVPGKQTSKGNHRIREFVSDYEPSEPGFCIHNIIMPQVTEYTSVLPSS 180

Db 121 GRMGSGTVPGKQTSKGNHRIREFVSDYEPSEPGFCIHNIIMPQVTEYTSVLPSS 180

QY 181 LSIDLNNATAPSTLELIRYLEPRDQWYDLSLYKPTMOLGKAFYGRKSKVYVNL 240

Db 181 LPDLNNATAPSTLELIRYLEPRDQWYDLSLYKPTMOLGKAFYGRKSKVYVNL 240

QY 241 LKEEVKLYSCTPRNFYSIREELKRTDTIFWPGCLVYKRCGNACCLHNCNEQCVPRK 300

Db 241 LKEEVKLYSCTPRNFYSIREELKRTDTIFWPGCLVYKRCGNACCLHNCNEQCVPRK 300

QY 301 VTKKYEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNMAG 345

Db 301 VTKKYEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRGNMAG 345

RESULT 4

US-09-265-686-2

Sequence 2, Application US/09265686

Patent No. 6455283

GENERAL INFORMATION:

APPLICANT: Ferrara, Napoleone

APPLICANT: Kuo, Sophia S.

TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1

FILE REFERENCE: P1122P2

CURRENT APPLICATION NUMBER: US/09/265,686

CURRENT FILING DATE: 1999-03-10

PRIOR APPLICATION NUMBER: US 09/040,220

PRIOR FILING DATE: 1998-03-17

PRIOR APPLICATION NUMBER: US 09/184,216

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 2

LENGTH: 345

TYPE: PRT

ORGANISM: Human

US-09-265-686-2

Query Match 90.2%; Score 1667; DB 4; Length 345;

Best Local Similarity 87.0%; Pred. No. 4,6e-175;

Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGQGTGTRAESNLSKQLQSDKEQNGVQDPRHRRVYVITSGNSIHS 60

Db 1 MSFGLLLTSALAGQGTGTRAESNLSKQFQSSNKEQNGVQDPRHRRVYVITSGNSIHS 60

QY 61 PKPHTYPRNMVLYWRVAVDENVRIQITFDERGLEDPEDDICKYDFVEVEEPPSDGTYL 120

Db 61 PREPHTYPRNTVLYWRVAVDENVRIQITFDERGLEDPEDDICKYDFVEVEEPPSDGTYL 120

QY 121 GRMGSGTVPGKQTSKGNHRIREFVSDYEPSEPGFCIHNIIMPQVTEYTSVLPSS 180

Db 121 GRMGSGTVPGKQTSKGNHRIREFVSDYEPSEPGFCIHNIIMPQVTEYTSVLPSS 180

QY 181 LSIDLNNATAPSTLELIRYLEPRDQWYDLSLYKPTMOLGKAFYGRKSKVYVNL 240

Db 181 LPDLNNATAPSTLELIRYLEPRDQWYDLSLYKPTMOLGKAFYGRKSKVYVNL 240

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	Best Local Similarity	43.55	Pred. No. 1.3e-73		
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QY	16 QRTGTRAESNLSSKLTQTSDEKQGVODPRHREAVTISGNGSIHSPFPTTPRNWLYW	75			
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Db	26 QRASIKALRNAN-----LRDSESNHLDLYQOEENIQVTSNGHWGSPRPNSYPRNLLLTW	81			
QY	76 RLAVADENVRQLTFDERFGLDEPDIDICKDYVEVEEPSDGS--VLGRMGSGSTYVPGK	133			
	: : : : : : : : : : : : : : : : : : : : : : : :				
Db	82 WLRS-OEKTRIQLSFDFQGLFEAEANDICRYDFEVEVEEVSSTYVYGRMGKHEIPRI	140			
QY	134 TSKGNHTRIRPSEYSEYSPSEPGCFIHSHII--MPOVTEFT-----SPSV	175			
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Db	141 TSKRNQIKITFKSDYTVAKGPFYITVSEVEDFOEPAESEFTNMESVTSFSGVSYHSPSI	200			
QY	176 LPPESSLIDLNNVTAFTSTLEELIRYLEPRMVDLSLYKPTWQLGKAFTLGKRSKY	235			
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Db	201 TDP-TLVADALDKVAIEDYIEDLTKKFNPNVSMQDDELLYDTPHNRGSY-HDRSK-	257			
QY	236 VNLMLKEVLYKSCTPRPNFSVSIREDLKRDTITFWPGCLLYVRGGNACACCLHNCEQ	295			
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Db	258 VDLRLNDVRYKRYCTPRNHSVNLREELKLTNAVEFPRLCLLYVRGGNCGGIVNMKSC	317			
QY	296 CVPRKRYTKKHYEQLRP---KITGVKLGHSLLTVLALEHNEEDCV	339			
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Db	318 CSSKTYAKKYAEVLYKFEGRKRRGKKANMALVDIODIHNERCCIC	364			

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Sequence 1 Application US/08572225
Patent No. 5807981
GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Hojima, Yoshio
APPLICANT: Li, Shi-Wu
APPLICANT: Sieron, Alexander
APPLICANT: Brenner, Mitch
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/572.225
FILING DATE: 13-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-572-225-1

Query Match 9.8%; Score 181; DB 1; Length 788;
Best Local Similarity 42.6%; Pred. NO. 8.8e-11;
Matches 46; Conservative 16; Mismatches 38; Indels 8; Gaps 5;

QY 55 NGSIHSPKPEPTTYRNWLVRLVAADENVNLTOTLFDREFGLEDEDDICKYDFVEVEE- 113
Db 401 NGSTISQPMPEPTYPNNKNCIMQVLAPTQ-YTISLQFD--FFETEGNDVCYIDFVEVRS- 456
QY 114 -PSDGSVLGRMGSGGTVPKGQTSKGNHIRIRFVSDSEFPSPGRCIHY 160
Db 457 LTADSKLHKFGCS-EKPEVITTSQYNNMRVFEKSDNTV-SKKGKRAHF 502

RESULT 10
US-08-872-757-2
Sequence 2, Application US/08872757
Patent No. 6258584
GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Hojima, Yoshio
APPLICANT: Li, Shi-Wu
APPLICANT: Sieron, Alexander
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
TITLE OF INVENTION: PROCESSES; METHODS AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York

```

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,757
FILING DATE: 10-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/609,187
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-028-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 730 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-872-757-2

Query Match 9.6%; Score 177.5; DB 4; Length 730;
Best Local Similarity 38.1%; Pred. No. 1.9e-10;
Matches 48; Conservative 18; Mismatches 45; Indels 15; Gaps 6;
QY 55 NGSIHSPKPHPTPRNNVLRVAVDENVRIOITFDERFGLDEPDICKYFVEVEE- 113
DB 599 NGSIHSPKPHPTPRNNVLRVAVDENVRIOITFDERFGLDEPDICKYFVEVEE- 113
QY 114 -PSDGSVLGRWCGSGTVPGKOTSGKNHIRIRFVSDDEFPEPGCFCHKYSIIMPOVETTS 172
DB 655 LTAHSLKHKFGCS-EKPEVITSOYNNMVEFKSDNTV-SKKGFAHF-----FSENR 705
QY 173 PSVLP 178
DB 706 PALQP 711

RESULT 11
US-09-374-135-6
Sequence 6, Application US/09374135
Patent No. 6277972
GENERAL INFORMATION:
APPLICANT: Afari, Daniel E.
APPLICANT: Hubert, Rene S.
APPLICANT: Leone, Kahen
APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND
FILE REFERENCE: 1703-017. US1
CURRENT APPLICATION NUMBER: US/09/374,135
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/095,982
PRIOR FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 101
TYPE: PRT
ORGANISM: Mouse
US-09-374-135-6

Query Match 9.5%; Score 175; DB 4; Length 101;
Best Local Similarity 42.1%; Pred. No. 1.5e-11;
Matches 45; Conservative 16; Mismatches 38; Indels 8; Gaps 5;
QY 56 GSIIHSPKPHPTPRNNVLRVAVDENVRIOITFDERFGLDEPDICKYFVEVEE- 113
DB 1 GSIIHSPKPHPTPRNNVLRVAVDENVRIOITFDERFGLDEPDICKYFVEVEE- 113
QY 114 PSDGSVLGRWCGSGTVPGKOTSGKNHIRIRFVSDDEFPEPGCFCHKYSIIMPOVETTS 172
DB 57 TADSKLHKFGCS-EKPEVITSOYNNMVEFKSDNTV-SKKGFAHF 101

RESULT 12
US-09-116-473-4
Sequence 4, Application US/09116473
Patent No. 6428965
GENERAL INFORMATION:
APPLICANT: Kolodkin, Alex
APPLICANT: Ginty, David
TITLE OF INVENTION: SEMAPHORIN RECEPTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,473
FILING DATE: 17-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/052,762
FILING DATE: 17-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.74973
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 922 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-116-473-4

Query Match 9.3%; Score 172; DB 4; Length 922;
Best Local Similarity 31.5%; Pred. No. 1.1e-09;
Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;
QY 2 LILGLLITSLAGORITRAESNLSSKLLSDSKDENGVQDPRHENVYISGSIHSP 61
DB 7 LILGLLITSLAGORITRAESNLSSKLLSDSKDENGVQDPRHENVYISGSIHSP 61
QY 62 KPHPTPRNNVLRVAVDENVRIOITFDERFGLDEPDICKYFVEVEE-EPSPGSV 119
DB 43 GYHSPKPHPTPRNNVLRVAVDENVRIOITFDERFGLDEPDICKYFVEVEE-EPSPGSV 119
QY 120 LGRWCGSGTVPGKOTSGKNHIRIRFVSDDEFPEPGCFCHKYSIIM-POVETTS 174
DB 100 LGRWCGSGTVPGKOTSGKNHIRIRFVSDDEFPEPGCFCHKYSIIM-POVETTS 174

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RESULT 13
US-08-936-135-6
; Sequence 6, Application US/08936135
; Patent No. 6034293
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: He, Zhigang
; APPLICANT: Chen, Hang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 923 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-936-135-6

Query Match
Best Local Similarity 9.1%; Score 169; DB 3; Length 923;
Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;

QY 2 LLLGLLLTSALAGQRTGTRAESNLSSKIQLSDDKQNGVQDPRHREVVTISGNGSIHSP 61
DB 7 LLCATLALALAG-----AFRSDKCG-----TKIENPGYLTSP 42
QY 62 KPHTYPRNNVWLRVAVDENVRIOITPDERGLEDPEDDICKYDVEV--EPPSGSV 119
DB 43 GYPHSHPSKCEWLIQAPPEYQRIIINFPHDLEDRD---CKYDVEYIDGENEGRL 99
QY 120 LGRWCGSGYVPGKQTSKGNHRIREFVDEYFPPSPGCIHYSIIM--POYLET-TSPS 174
DB 100 WGFECGR-IPSPVSSGPFILFKFVSD-YETHGAGSIRKELFKRPECQNTAFT 155

RESULT 14
US-08-872-757-4
; Sequence 4, Application US/08872757
; Patent No. 6258584
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Alexander
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
; TITLE OF INVENTION: PROCESSES, METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 6
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,757
; FILING DATE: 10-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,187
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-028-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 986 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-872-757-4

Query Match
Best Local Similarity 9.1%; Score 168; DB 4; Length 986;
Matches 44; Conservative 16; Mismatches 40; Indels 8; Gaps 5;

QY 55 NGSIHSPKPHYTPRNNVWLRVAVDENVRIOITPDERGLEDPEDDICKYDVEVEE- 113
DB 599 NGSLISRGWPKPEYPPNKNQWLAPQO-YRISLQFD---FFTEGNDVCKYDVEVRSG 654
QY 114 -PSDGSVIGRWCGSGYVPGKQTSKGNHRIREFVDEYFPPSPGCIHY 160
DB 655 LTADSKLHGKFCGS-EKPEVITSOYNNMRYEFSKDNIV-SKKGKAEH 700

RESULT 15
US-08-866-650-3
; Sequence 3, Application US/08866650
; Patent No. 5939321
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S
; APPLICANT: Takahara, Kazuhiko
; APPLICANT: Hoffman, Guy G
; TITLE OF INVENTION: Mammalian Tolloid-Like Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Plinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,650
; FILING DATE:
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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 08:57:36 ; Search time 33.5 Seconds
(without alignments)
1372.283 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLLLTSLAGQRTGT.....DVALEHHECDCCVCRGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1848	100.0	345	21	Mouse zvegfg3, SRQ
3	1848	100.0	345	21	Mouse zvegfg3, SRQ
4	1848	100.0	345	22	Mouse zvegfg3, SRQ
5	1848	100.0	345	23	Mouse zvegfg3, SRQ
6	1848	100.0	345	23	Mouse zvegfg3, SRQ
7	1848	100.0	345	20	Human VEGF-E prote
8	1667	90.2	345	20	Human PRO200 prote
9	1667	90.2	345	20	Human VEGF-E prote
10	1667	90.2	345	20	Human VEGF-E prote

11	1667	90.2	345	21	AA1980.DAT
12	1667	90.2	345	21	AA1981.DAT
13	1667	90.2	345	21	AA1982.DAT
14	1667	90.2	345	21	AA1983.DAT
15	1667	90.2	345	21	AA1984.DAT
16	1667	90.2	345	21	AA1985.DAT
17	1667	90.2	345	21	AA1986.DAT
18	1667	90.2	345	21	AA1987.DAT
19	1667	90.2	345	21	AA1988.DAT
20	1667	90.2	345	21	AA1989.DAT
21	1667	90.2	345	21	AA1990.DAT
22	1667	90.2	345	21	AA1991.DAT
23	1667	90.2	345	21	AA1992.DAT
24	1667	90.2	345	22	AA1993.DAT
25	1667	90.2	345	22	AA1994.DAT
26	1667	90.2	345	22	AA1995.DAT
27	1667	90.2	345	22	AA1996.DAT
28	1667	90.2	345	22	AA1997.DAT
29	1667	90.2	345	22	AA1998.DAT
30	1667	90.2	345	22	AA1999.DAT
31	1667	90.2	345	22	AA2000.DAT
32	1667	90.2	345	22	AA2001.DAT
33	1667	90.2	345	23	AA2002.DAT
34	1667	90.2	345	23	AA2003.DAT
35	1667	90.2	345	23	AA2004.DAT
36	1667	90.2	345	21	AA1980.DAT
37	1667	90.2	345	21	AA1981.DAT
38	1667	90.2	345	21	AA1982.DAT
39	1667	90.2	345	21	AA1983.DAT
40	1667	90.2	345	21	AA1984.DAT
41	1667	90.2	345	21	AA1985.DAT
42	1667	90.2	345	21	AA1986.DAT
43	1667	90.2	345	21	AA1987.DAT
44	1667	90.2	345	21	AA1988.DAT
45	1667	90.2	345	21	AA1989.DAT

ALIGNMENTS

RESULT 1	AA1980.DAT	AA1981.DAT	AA1982.DAT	AA1983.DAT	AA1984.DAT	AA1985.DAT	AA1986.DAT	AA1987.DAT	AA1988.DAT	AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT
AA1980.DAT	AA1981.DAT	AA1982.DAT	AA1983.DAT	AA1984.DAT	AA1985.DAT	AA1986.DAT	AA1987.DAT	AA1988.DAT	AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT
AA1981.DAT	AA1982.DAT	AA1983.DAT	AA1984.DAT	AA1985.DAT	AA1986.DAT	AA1987.DAT	AA1988.DAT	AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT
AA1982.DAT	AA1983.DAT	AA1984.DAT	AA1985.DAT	AA1986.DAT	AA1987.DAT	AA1988.DAT	AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT
AA1983.DAT	AA1984.DAT	AA1985.DAT	AA1986.DAT	AA1987.DAT	AA1988.DAT	AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT
AA1984.DAT	AA1985.DAT	AA1986.DAT	AA1987.DAT	AA1988.DAT	AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT
AA1985.DAT	AA1986.DAT	AA1987.DAT	AA1988.DAT	AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT
AA1986.DAT	AA1987.DAT	AA1988.DAT	AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT
AA1987.DAT	AA1988.DAT	AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT
AA1988.DAT	AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT
AA1989.DAT	AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT
AA1990.DAT	AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT	AA2013.DAT
AA1991.DAT	AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT	AA2013.DAT	AA2014.DAT
AA1992.DAT	AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT	AA2013.DAT	AA2014.DAT	AA2015.DAT
AA1993.DAT	AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT	AA2013.DAT	AA2014.DAT	AA2015.DAT	AA2016.DAT
AA1994.DAT	AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT	AA2013.DAT	AA2014.DAT	AA2015.DAT	AA2016.DAT	AA2017.DAT
AA1995.DAT	AA1996.DAT	AA1997.DAT	AA1998.DAT	AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT	AA2013.DAT	AA2014.DAT	AA2015.DAT	AA2016.DAT	AA2017.DAT	AA2018.DAT
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AA1999.DAT	AA2000.DAT	AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT	AA2013.DAT	AA2014.DAT	AA2015.DAT	AA2016.DAT	AA2017.DAT	AA2018.DAT	AA2019.DAT	AA2020.DAT	AA2021.DAT	AA2022.DAT
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AA2001.DAT	AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT	AA2013.DAT	AA2014.DAT	AA2015.DAT	AA2016.DAT	AA2017.DAT	AA2018.DAT	AA2019.DAT	AA2020.DAT	AA2021.DAT	AA2022.DAT	AA2023.DAT	AA2024.DAT
AA2002.DAT	AA2003.DAT	AA2004.DAT	AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT	AA2013.DAT	AA2014.DAT	AA2015.DAT	AA2016.DAT	AA2017.DAT	AA2018.DAT	AA2019.DAT	AA2020.DAT	AA2021.DAT	AA2022.DAT	AA2023.DAT	AA2024.DAT	AA2025.DAT
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AA2005.DAT	AA2006.DAT	AA2007.DAT	AA2008.DAT	AA2009.DAT	AA2010.DAT	AA2011.DAT	AA2012.DAT	AA2013.DAT	AA2014.DAT	AA2015.DAT													

DR WPI: 2000-687541/67.
 DR N-PSDB; AAC81583.
 XX Growth factor homologs and the nucleic acids that encode them, useful
 PT e.g. for treating liver damage, ischemia, multiple sclerosis and
 PT Alzheimer's disease -
 XX
 XX Disclosure; Page 130-131, 143pp: English.
 XX
 XX The invention relates to the human growth factor homologue zvegf4
 CC (AAB8653), and nucleic acids encoding it (AAC8155). Zvegf4 is a member
 CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
 CC growth factor) family. Zvegf4 has a growth factor domain (AAB8654)
 CC characterised by a PDGF cystine knot structure, and a CUB domain
 CC (AAB8655) which has a beta barrel structure. Zvegf4 has PDGF-like
 CC activity, having mitogenic activity on fibroblasts, vascular smooth
 CC muscle cells and pericytes, and has also been shown to stimulate bone
 CC growth. The invention also relates to fusion proteins comprising human
 CC zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3
 CC fusions; expression constructs and host cells comprising human zvegf4
 CC nucleic acids; the recombinant expression of human zvegf4; an antibody
 CC which binds to human zvegf4 or a fragment thereof; a method of activating
 CC a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a
 CC method of modulating the proliferation, differentiation, migration or
 CC metabolism of bone cells, comprising exposing bone cells to
 CC zvegf4-derived polypeptides; and a method of detecting a genetic
 CC abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived
 CC fragments may be used to stimulate tissue development or repair, or
 CC cellular differentiation or proliferation. They are particularly used for
 CC the treatment or repair of liver damage, and may also be used to
 CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
 CC multiple sclerosis). Due to their osteogenic activity, they may be used
 CC in the treatment of periodontal disease and fractures. They may also be
 CC used to enhance expansion and mobilisation of haematopoietic stem cells
 CC and endothelial precursor stem cells, which may be useful in the
 CC treatment of ischaemia, in wound healing, and in the modulation of the
 CC immune system. The present sequence represents mouse zvegf3.
 CC
 XX
 XX Sequence 345 AA:
 SQ
 Query Match 100.0%; Score 1848; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 6,4e-182;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC AAY96861;
 XX
 XX 26-SEP-2000 (first entry)
 DT
 XX
 DE Murine vascular endothelial growth factor homologue, ZVEGF3.
 XX
 XX Vascular endothelial growth factor; homologue: zvegf3; CUB domain;
 KM Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;
 KM chromosome 4q28.3; cytosolic; anti-psoriatic; anti-inflammatory;
 KM anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic;
 KM vulnery.
 XX
 XX Mus musculus.
 OS
 XX
 PN M0200034474-A2.
 PD
 PD 15-JUN-2000.
 PD
 PD 07-DEC-1999; 99MO-US28968.
 PF
 PF 07-DEC-1999; 99MO-US28968.
 PR
 PR 07-DEC-1999; 98US-0207120.
 PR 06-JUL-1999; 99US-0142576.
 PR 21-OCT-1999; 99US-0161653.
 PR 12-NOV-1999; 99US-0165255.
 PR
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
 PI Gilbertson DG, West JW;
 PI
 DR WPI: 2000-423420/36.
 DR N-PSDB; AAA51527.
 XX
 XX Novel zvegf3 polypeptides and nucleotides encoding them useful for
 PT stimulating growth of smooth muscle cells and fibroblasts comprising an
 PT epitope bearing portion of a specific amino acid sequence
 XX
 XX Claim 1; Page 169-170; 173pp: English.
 PS
 PS
 XX This shows a murine ZVEGF3 a novel vascular endothelial growth factor
 CC homologue. Polypeptides comprising an epitope-bearing portion human or
 CC murine ZVEGF3 are claimed. The growth factors comprise a growth factor
 CC domain and a CUB domain (generic sequence motifs are shown in AAY96859
 CC and AAY96860). The growth factor domain is characterized by an
 CC arrangement of cysteine residues and beta-strands that is characteristic
 CC of the "cysteine knot" structure of the platelet-derived growth factor
 CC (PDGF) family. The CUB domain shows homology to CUB domains in
 CC neuropilins, human bone morphogenetic protein-1, porcine seminal plasma
 CC protein, bovine acidic seminal fluid protein and Xenopus laevis
 CC tolloid-like protein. Structural analysis and homology predict that
 CC ZVEGF3 polypeptides complex with a second polypeptide to form multimeric
 CC proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3.
 CC ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth
 CC muscle cells, for activating cell surface PDGF-alpha receptor and for
 CC inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is
 CC useful for regulating (post-development) organ growth, regeneration and
 CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3
 CC antagonists are useful for treating cancer, rheumatoid arthritis,
 CC diabetic retinopathy, ischemic limb disease, peripheral vascular
 CC disease, myocardial ischemia, vascular intimal hyperplasia,
 CC atherosclerosis, wound healing, chronic liver disease and haemangioma
 CC formation. ZVEGF3 can also be used to modulate neurite growth and
 CC development of the nervous system, and for treating neurodegenerative
 CC diseases.
 XX
 XX Sequence 345 AA:
 SQ
 Query Match 100.0%; Score 1848; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 6,4e-182;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MLLGLLLTSALAGORTGTRAESNLSKQLQSSDKQNGVQDPRIHRYVTISGNGSIHS 60
 QY 61 PKRPHTYPRNMVLWVRVAVDENVRIOQLFDERFGLEDDEDICKYDFVEEPPSDGSYL 120
 Db 61 PKRPHTYPRNMVLWVRVAVDENVRIOQLFDERFGLEDDEDICKYDFVEEPPSDGSYL 120
 QY 121 GRMGSGTVPGKOTSGKNHRIREFVDEYPPSEPGCIHYSIIMPVETTSVLPSS 180
 Db 121 GRMGSGTVPGKOTSGKNHRIREFVDEYPPSEPGCIHYSIIMPVETTSVLPSS 180
 QY 181 LSLDLLNNVATFASLEELIRYLEPDRMOVDLSLKPMTQLGKAFLYGKSKVNNLN 240
 Db 181 LSLDLLNNVATFASLEELIRYLEPDRMOVDLSLKPMTQLGKAFLYGKSKVNNLN 240
 QY 241 LKEEVKLYSCTPRNFVSITREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPRK 300
 Db 241 LKEEVKLYSCTPRNFVSITREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPRK 300
 QY 301 VTKKHEVLDLRPKTGKGLHKSITDVALEHHECCDVCGRNAG 345
 Db 301 VTKKHEVLDLRPKTGKGLHKSITDVALEHHECCDVCGRNAG 345

RESULT 3

AAE0998
ID AAE0998 standard; Protein; 345 AA.

AAE0998
AC AAE0998;

DT 25-JUL-2000 (first entry)

DE A murine platelet-derived growth factor C (PDGF-C).

KM Platelet-derived growth factor C; PDGF-C; cell proliferation;
 KM growth factor; heparin; connective tissue; wound healing; VEGF-F;
 KM fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
 KM chorioarcinoma; Wilms tumour; megakaryoblastic leukaemia;
 KM lung carcinoma; erythroleukemia; tissue remodelling.

OS Mus sp.

PN WO200018212-A2.

PD 06-APR-2000.

PF 30-SEP-1999; 99WO-US22668.

PR 30-SEP-1998; 98US-0102461.

PR 12-NOV-1998; 98US-0108109.

PR 03-DEC-1998; 98US-0110749.

PR 18-DEC-1998; 98US-0113002.

PR 21-MAY-1999; 99US-0135426.

PR 15-JUL-1999; 99US-0144022.

XX (LUDM-) LUDMIG INST CANCER RES.

PA (UYHE-) UNIV HELSINKI LICENSING LTD.

PI Eriksson U, Aase K, Lee X, Ponten A, Urtela M, Altalo K;

PI Oestman A, Heldin C, Betsholtz C;

XX WPI: 2000-292954/25.

DR N-PSDB; AAA12525.

PT Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,

PT receptor - growth and motility of cells expressing the PDGF-C

XX Claim 27; Fig 6; 135pp; English.

CC The present sequence represents murine platelet-derived growth factor C

CC (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the

CC ability to stimulate and enhance proliferation or differentiation,

CC and/or growth or motility of cells expressing a PDGF-C receptor.

CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
 CC proliferation, preferably in combination with one other growth factor
 CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
 CC be used for stimulating connective tissue or wound healing. The
 CC PDGF-C polypeptide can be enzymatically processed to generate the active
 CC truncated form of PDGF-C and used to regulate the receptor-binding
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
 CC chorioarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
 CC and erythroleukemia, can be identified by testing for expression of
 CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
 CC remodelling during invasion of tumour cells into a normal population of
 CC cells. Antagonists can also be used to treat fibrotic conditions,
 CC especially found in the lung, kidney or liver.

SQ Sequence 345 AA:

Query Match 100.0%; Score 1848; DB 21; Length 345;

Best local Similarity 100.0%; Pred. No. 6.4e-182;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAESNLSKQLQSSDKQNGVQDPRIHRYVTISGNGSIHS 60

Db 1 MLLGLLLTSALAGORTGTRAESNLSKQLQSSDKQNGVQDPRIHRYVTISGNGSIHS 60

QY 61 PKRPHTYPRNMVLWVRVAVDENVRIOQLFDERFGLEDDEDICKYDFVEEPPSDGSYL 120

Db 61 PKRPHTYPRNMVLWVRVAVDENVRIOQLFDERFGLEDDEDICKYDFVEEPPSDGSYL 120

QY 121 GRMGSGTVPGKOTSGKNHRIREFVDEYPPSEPGCIHYSIIMPVETTSVLPSS 180

Db 121 GRMGSGTVPGKOTSGKNHRIREFVDEYPPSEPGCIHYSIIMPVETTSVLPSS 180

QY 181 LSLDLLNNVATFASLEELIRYLEPDRMOVDLSLKPMTQLGKAFLYGKSKVNNLN 240

Db 181 LSLDLLNNVATFASLEELIRYLEPDRMOVDLSLKPMTQLGKAFLYGKSKVNNLN 240

QY 241 LKEEVKLYSCTPRNFVSITREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPRK 300

Db 241 LKEEVKLYSCTPRNFVSITREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPRK 300

QY 301 VTKKHEVLDLRPKTGKGLHKSITDVALEHHECCDVCGRNAG 345

Db 301 VTKKHEVLDLRPKTGKGLHKSITDVALEHHECCDVCGRNAG 345

RESULT 4

AAE00998
ID AAE00998 standard; Protein; 345 AA.

AC AAE00998;

DT 04-JUL-2001 (first entry)

DE Mouse zveg3 protein.

KM Mouse; zveg3 antagonist; cell proliferation; stellate cell activation;
 KM extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
 KM platelet-derived growth factor; PDGF; vascular endothelial growth factor;
 KM VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
 KM chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
 KM diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
 KM asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
 KM pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
 KM bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
 KM fibroproliferative disorder.

XX Mus musculus.

OS WO200128586-A1.

PN

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XX PD 26-APR-2001.
XX PF 23-OCT-2000: 2000MO-US29270.
XX PR 21-OCT-1999: 990US-016153.
XX PR 12-NOV-1999: 990US-0165255.
XX PR 01-AUG-2000: 2000US-0222223.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI GILBERTSON DG:
XX DR WPI: 2001-300278/31.
XX N-PSDB: AAD04650.
XX PT Use of zvegf3 antagonist for reducing fibroproliferative disorder of
XX PT kidney, liver and bone, reducing extracellular matrix production,
XX PT treating fibrosis or reducing stellate cell activation in mammal
XX PS Example 2; Fig 2; 70pp; English.
XX CC The patent discloses materials and methods for reducing cell
XX CC proliferation or extracellular matrix production, treating fibrosis and
XX CC reducing stellate cell activation in a mammal. The method comprises
XX CC administering a composition containing a zvegf3 antagonist in combination
XX CC with a delivery vehicle. The zvegf3 is a protein that is structurally
XX CC related to platelet-derived growth factor (PDGF) and the vascular
XX CC endothelial growth factors (VEGF). The zvegf3 protein is also designated
XX CC as "VEGF-R" and "PDGF-C". The zvegf3 antagonist is useful to block the
XX CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
XX CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
XX CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and
XX CC alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as
XX CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
XX CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
XX CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
XX CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,
XX CC fibrotic disorders of pancreas, fibroproliferative disorders of the
XX CC vasculature such as transplant vasculopathy and fibroproliferative
XX CC disorders of the bone such as osteopetrosis and hyperostosis.
XX CC The present sequence is mouse zvegf3 protein.
XX SQ Sequence 345 AA:

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Query Match 100.0%; Score 1848; DB 22; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.4e-182;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLLGLLLLSALAGORTGTRAESNLSKQLSSDKONGVOPRHRVVTISGNSIHS 60
DB 1 MLLGLLLLSALAGORTGTRAESNLSKQLSSDKONGVOPRHRVVTISGNSIHS 60
QY 61 PKRPHRYPRMNVLMVRLVAVDENVRIDLTDERGLEDPEDDICKDFVEVEEPPSDG 120
DB 61 PKRPHRYPRMNVLMVRLVAVDENVRIDLTDERGLEDPEDDICKDFVEVEEPPSDG 120
QY 121 GRMGSGTGVGKOTSKGNHRIKRVFSDPEPSPGFCIHSTIMPQVETTSVPLPSS 180
DB 121 GRMGSGTGVGKOTSKGNHRIKRVFSDPEPSPGFCIHSTIMPQVETTSVPLPSS 180
QY 181 LSLDLLNNAVTAESTLEELIRYLEPDRMOYDLISLKPQWLLGKAFLYGKRSKVNL 240
DB 181 LSLDLLNNAVTAESTLEELIRYLEPDRMOYDLISLKPQWLLGKAFLYGKRSKVNL 240
QY 241 LKEEVKILSYSTPRNFVSISIEELKRTDTIPWPGCLLYKRCGGACCLHNCNECQVPRK 300
DB 241 LKEEVKILSYSTPRNFVSISIEELKRTDTIPWPGCLLYKRCGGACCLHNCNECQVPRK 300
QY 301 VTKKHYEVLQLRPTGVKGLHKSLLTDVALHHEECDCVCGNAGG 345
DB 301 VTKKHYEVLQLRPTGVKGLHKSLLTDVALHHEECDCVCGNAGG 345

```

```

RESULT 5
AAB47890
ID AAB47890 standard; Protein; 345 AA.
XX AC AAB47890:
XX DT 16-MAY-2002 (first entry)
XX DE Mouse zvegf3.
XX KW Human; mouse; zvegf3; zvegf4; platelet derived growth factor;
XX KW PDGF; homolog; growth; bone; ligament; cartilage; proliferation;
XX KW osteoblast; chondrocyte; bony defect; fracture; bone graft;
XX KW implant; periodontal pocket; osteoclast; bone marrow stem cell;
XX OS Mus musculus.
XX PN US2002004225-A1.
XX PD 10-JAN-2002.
XX PF 29-MAR-2001; 2001US-0823033.
XX PR 07-DEC-1998: 98US-111173P.
XX PR 06-JUL-1999: 99US-142576P.
XX PR 21-OCT-1999: 99US-161653P.
XX PR 12-NOV-1999: 99US-165255P.
XX PR 31-MAR-2000: 2000US-193723P.
XX PR 07-DEC-1999: 99US-0457066.
XX PA (HART/) HART C E.
XX PA (GILB/) GILBERTSON D G.
XX PI Hart CE, Gilbertson DG:
XX DR WPI: 2002-171026/22.
XX DR N-PSDB: AAI72444.
XX PT Promoting growth of bone, ligament or cartilage in a mammal, involves
XX PT administering to the mammal a protein which comprises growth factor
XX PT domain of zvegf3 protein, a homolog of platelet-derived growth factor
XX PS Claim 1; Page 19-20; 31pp; English.
XX CC The sequences given in AAB4789-90 represent human and mouse zvegf3,
XX CC respectively. zvegf3 is a platelet derived growth factor (PDGF) homolog
XX CC and it was used in the method of the invention for promoting growth of
XX CC bone, ligament or cartilage and stimulating proliferation of osteoblasts
XX CC or chondrocytes in a mammal. The proteins used were preferably a dimeric
XX CC protein of residues 235-345 of human zvegf3 or all of the mouse zvegf3
XX CC protein, with a delivery vehicle. The method of th invention is useful
XX CC for promoting growth of bone, ligament or cartilage in a mammal, where
XX CC the composition is administered at a site of a bony defect, preferably
XX CC a fracture, bone graft site, implant site, or periodontal pocket, and
XX CC for stimulating proliferation of osteoblasts or chondrocytes in a
XX CC mammal. It is further useful for promoting proliferation of osteoblasts,
XX CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone
XX CC marrow stem cells are harvested from a patient prior to culture. The
XX CC method is therefore useful for treating osteoporosis.
XX SQ Sequence 345 AA:

```

```

Query Match 100.0%; Score 1848; DB 23; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.4e-182;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGLLLLSALAGORTGTRAESNLSKQLSSDKONGVOPRHRVVTISGNSIHS 60
DB 1 MLLGLLLLSALAGORTGTRAESNLSKQLSSDKONGVOPRHRVVTISGNSIHS 60

```

QY 61 PKFPHTYPRNNMVLVWRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFEVEEPEPSDGSVL 120
 |||||
 DB 61 PKFPHTYPRNNMVLVWRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFEVEEPEPSDGSVL 120
 |||||
 QY 121 GWMCGSSGIVPGKQTSKGNHIRIRFVSDEYFPESEPGFCHYSTIMPOVETTSPSVLPSS 180
 |||||
 DB 121 GWMCGSSGIVPGKQTSKGNHIRIRFVSDEYFPESEPGFCHYSTIMPOVETTSPSVLPSS 180
 |||||
 QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRMQVDSDSLYKPTWOLGKAFLYGKSKSVVNLNL 240
 |||||
 DB 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRMQVDSDSLYKPTWOLGKAFLYGKSKSVVNLNL 240
 |||||
 QY 241 LKEEVKLYSCPTFRNFSVSIREELKRTDTTFWPGCLLYKRCGNCACCLHNCNECCVPRK 300
 |||||
 DB 241 LKEEVKLYSCPTFRNFSVSIREELKRTDTTFWPGCLLYKRCGNCACCLHNCNECCVPRK 300
 |||||
 QY 301 VTKKTHEVQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345
 |||||
 DB 301 VTKKTHEVQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345
 |||||

RESULT 6

AAEI3213
 ID AAEI3213 standard; Protein: 345 AA.

AC AAEI3213;
 DT 12-FEB-2002 (first entry)

XX Mouse platelet-derived growth factor (PDGF-C) protein.

DE Mouse platelet-derived growth factor (PDGF-C) protein.

KW Mouse; transgenic animal; platelet derived growth factor C; PDGF-C;
 cardiac hypertrophy; fibrosis.

KW cardiac hypertrophy; fibrosis.

OS Mus sp.

PN WO200172132-A1.

PD 04-OCT-2001.

PF 28-MAR-2001; 2001WO-US09855.

PR 28-MAR-2000; 2000US-192507P.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Eriksson U, Li X, Ponten A, Aase K, Li H;

DR WPI: 2002-010700/01.

XX A transgenic animal over-expressing platelet derived growth factor C is
 PT useful to study and find therapy for disease associated with PDGF-C
 PT over-expression, including cardiac hypertrophy and fibrosis

PS Example 4: Page 42-43; 48pp; English.

XX The patent discloses a method for producing a transgenic, non-human
 CC animal over-expressing a platelet derived growth factor C (PDGF-C),
 CC or its functional fragment or analogue. The method involves introducing
 CC a transgenic PDGF-C DNA into a cell of a non-human animal, introducing
 CC the cell into a non-human animal and allowing the cell to develop into
 CC a transgenic, non-human animal. The transgenic animal is useful as a
 CC model to study disease states characterised by over-expression of PDGF-C
 CC and to find therapy for those diseases, particularly hypertrophy and
 CC fibrosis in various organs including the heart. The present sequence
 CC is PDGF-C protein from mouse.

XX Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 23; Length 345;
 Best Local Similarity 100.0%; Pred. No. 6,4e-182;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLLLLLTSALAGQRTGTRAESNLSSKQLQSDKEQNGVODPRHHERVYITSGNGSIHS 60
 |||||
 DB 1 MLLLLLLTSALAGQRTGTRAESNLSSKQLQSDKEQNGVODPRHHERVYITSGNGSIHS 60
 |||||
 QY 61 PKFPHTYPRNNMVLVWRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFEVEEPEPSDGSVL 120
 |||||
 DB 61 PKFPHTYPRNNMVLVWRLVAVDENVRIOQLTFDERFGLDEPEDDICKYDFEVEEPEPSDGSVL 120
 |||||
 QY 121 GWMCGSSGIVPGKQTSKGNHIRIRFVSDEYFPESEPGFCHYSTIMPOVETTSPSVLPSS 180
 |||||
 DB 121 GWMCGSSGIVPGKQTSKGNHIRIRFVSDEYFPESEPGFCHYSTIMPOVETTSPSVLPSS 180
 |||||
 QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRMQVDSDSLYKPTWOLGKAFLYGKSKSVVNLNL 240
 |||||
 DB 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRMQVDSDSLYKPTWOLGKAFLYGKSKSVVNLNL 240
 |||||
 QY 241 LKEEVKLYSCPTFRNFSVSIREELKRTDTTFWPGCLLYKRCGNCACCLHNCNECCVPRK 300
 |||||
 DB 241 LKEEVKLYSCPTFRNFSVSIREELKRTDTTFWPGCLLYKRCGNCACCLHNCNECCVPRK 300
 |||||
 QY 301 VTKKTHEVQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345
 |||||
 DB 301 VTKKTHEVQLRPKTVGKGLHKSITDVALEHHEECDCVCRGNAGG 345
 |||||

RESULT 7

AAV33679
 ID AAV33679 standard; Protein: 345 AA.

AC AAV33679;
 DT 11-JAN-2000 (first entry)

XX Human VEGF-E protein.

DE Human VEGF-E protein.

XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;
 KW treatment; cardiovascular disorder; endothelial disorder; therapy;
 KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
 KW angiogenic disorder; age-related macular degeneration; vascular disease;
 KW neovascularization; tumor; gene mapping.

OS Homo sapiens.

PN WO9947677-A2.

PD 23-SEP-1999.

PF 10-MAR-1999; 99WO-US05190.

PR 17-MAR-1998; 98US-0040220.

PR 02-NOV-1998; 98US-0184216.

PA (GETH) GENENTECH INC.

PI Ferrara N, Kuo SS;

DR WPI: 1999-580306/49.

DR N-PSDB: AA223691.

XX New growth factor polypeptide useful for treating cardiovascular or
 PT endothelial disorders, e.g. cardiac hypertrophy
 PT endothelial disorders, e.g. cardiac hypertrophy

PS Claim 1: Fig 2: 122pp; English.

XX This invention describes the isolation of a novel human vascular
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
 CC therapeutic, vulnerer and cardiant activity. VEGF-E can be administered
 CC therapeutically, especially by expressing encoding polynucleotides, to
 CC treat cardiovascular or endothelial disorders in mammals, especially
 CC humans. It is useful in wound repair and tissue generation and
 CC regeneration, and may especially be used to treat cardiac hypertrophy
 CC It can be combined with a carrier in pharmaceutical compositions, which
 CC can be administered to treat disorders as above. VEGF-E can be used to

PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
XX
PA (GETH) GENENTECH INC.
XX
XX PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX DR WPI: 1999-551358/46.
XX N-PSDB; AAZ34296.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
XX PS Claim 12; Fig 207; 530pp; English.
XX
XX CC The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AAZ33891 to
XX AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
XX
SQ Sequence 345 AA:
Query Match 90.2%; Score 1667; DB 20; Length 345;
Best Local Similarity 87.0%; Pred. No. 3.2e-163;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
YY 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVODPRHERVYTISGNSIHS 60
DB 1 MSIFGLLLTALAGROGTQAESNLSSKQFQSSNKEONGVODPOHERITVSTNGSIHS 60
YY 61 PREPHYPRNNMVLWRLVAVDENVRIOQLFDERFGLDEPEDDICKYDFVEVEEPPSDGSVYL 120
DB 61 PREPHYPRNNMVLWRLVAVDENVRIOQLFDERFGLDEPEDDICKYDFVEVEEPPSDGTTIL 120
YY 121 GRMGSGTVPKGQTSKGNHRIREFVSDEYFPPSPGFCIHYNITVMPQTEAVSPSVLPESA 180
DB 121 GRMGSGTVPKGQTSKGNHRIREFVSDEYFPPSPGFCIHYNITVMPQTEAVSPSVLPESA 180
YY 181 LSLDLLNNAVTAFTSEELIRYLEPDRMOVDLSLYKPTWOLGKAFVYGGKSKVYNLNL 240
DB 181 LSLDLLNNAVTAFTSEELIRYLEPDRMOVDLSLYKPTWOLGKAFVYGGKSKVYNLNL 240
YY 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFMPGCLLVKRCGNGACCLHNCNCCQCVPRK 300
DB 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFMPGCLLVKRCGNGACCLHNCNCCQCVPRK 300
YY 301 VTKKHYEVLQLRPKTVGKLIHNSLTDVALEHNEECDCVCRGNAGG 345
DB 301 VTKKHYEVLQLRPKTVGKLIHNSLTDVALEHNEECDCVCRGNAGG 345
RESULT 9
AA30023

ID AAY30023 standard; Protein; 345 AA.
XX
XX AC AAY30023;
XX
XX DT 11-OCT-1999 (first entry)
XX
XX DE Human vascular endothelial growth factor related protein.
XX
XX KW Vascular endothelial growth factor related protein; VEGF-R protein;
XX tissue growth inhibition; tumour growth; cancer; tissue growth;
XX angiogenesis; coronary artery blockage.
XX
XX OS Homo sapiens.
XX
XX PN MO9937671-A1.
XX
XX PD 29-JUL-1999.
XX
XX PF 26-JAN-1999; 99WO-US01574.
XX
XX PR 31-AUG-1998; 98US-0098548.
XX PR 27-JAN-1998; 98US-0072635.
XX PR 05-JUN-1998; 98US-0088089.
XX PR 24-JUN-1998; 98US-0090544.
XX
XX PA (ELIL) LILLY & CO ELI.
XX
XX PI Dou S, Na S, Song HY;
XX
XX DR WPI: 1999-458680/38.
XX N-PSDB; AAX86352.
XX
PT A vascular endothelial growth factor related protein and related
PT polynucleotide, useful for identifying antagonists and binding
PT compounds
XX
XX PS Claim 1; Page 56-58; 62pp; English.
XX
XX CC The present sequence represents a vascular endothelial growth factor
XX related (VEGF-R) protein. VEGF-R can be used in assays to identify
XX compounds that bind to it or that antagonize its activity. VEGF-R
XX antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
XX tissue growth. This is useful for inhibiting tumour growth and for
XX treating cancer. VEGF-R itself can be used to stimulate tissue
XX growth, angiogenesis and to treat coronary artery blockage. The
XX VEGF-R coding sequence can be used for the recombinant production of
XX the VEGF-R protein.
XX
SQ Sequence 345 AA:
Query Match 90.2%; Score 1667; DB 20; Length 345;
Best Local Similarity 87.0%; Pred. No. 3.2e-163;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
YY 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVODPRHERVYTISGNSIHS 60
DB 1 MSIFGLLLTALAGROGTQAESNLSSKQFQSSNKEONGVODPOHERITVSTNGSIHS 60
YY 61 PREPHYPRNNMVLWRLVAVDENVRIOQLFDERFGLDEPEDDICKYDFVEVEEPPSDGSVYL 120
DB 61 PREPHYPRNNMVLWRLVAVDENVRIOQLFDERFGLDEPEDDICKYDFVEVEEPPSDGTTIL 120
YY 121 GRMGSGTVPKGQTSKGNHRIREFVSDEYFPPSPGFCIHYNITVMPQTEAVSPSVLPESA 180
DB 121 GRMGSGTVPKGQTSKGNHRIREFVSDEYFPPSPGFCIHYNITVMPQTEAVSPSVLPESA 180
YY 181 LSLDLLNNAVTAFTSEELIRYLEPDRMOVDLSLYKPTWOLGKAFVYGGKSKVYNLNL 240
DB 181 LSLDLLNNAVTAFTSEELIRYLEPDRMOVDLSLYKPTWOLGKAFVYGGKSKVYNLNL 240
YY 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFMPGCLLVKRCGNGACCLHNCNCCQCVPRK 300
DB 241 LKEEVLYSCTPRNFSVSIREELKRTDTTFMPGCLLVKRCGNGACCLHNCNCCQCVPRK 300

CC promoting wound healing or stimulating smooth muscle growth by
 CC administering a platelet-derived growth factor (PDGF) related protein,
 CC designated Lp8 or its analogue. Also described is a method of slowing
 CC the progress of atherosclerosis or treating atherosclerosis comprising
 CC the administration of an Lp8 antagonist. The method is useful for
 CC enhancing tissue growth, promoting wound healing and stimulating smooth
 CC muscle growth. Antagonists of Lp8 are useful for treating
 CC atherosclerosis. The present sequence represents human Lp8, which is
 CC also called VEGFh.

XX Sequence 345 AA:

Query Match 90.2%; Score 1667; DB 21; Length 345;

Best Local Similarity 87.0%; Pred. No. 3.2e-163;

Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGORTGTRAESNLSSKQLQSSDKQNGVODPRHERVTTSGNGSIHS 60
 DB 1 MSLLFGLLLTSLAGORGTQAESNLSSKFQSSNKEQNGVODPOHERITIVSTNGSIHS 60
 QY 61 PKRPHTYPRNNMVLWRLVAVDENVRITQLTFDERFGLDEPEDDICKYDFVEVEPSPGSVYL 120
 DB 61 PKRPHTYPRNNMVLWRLVAVDENVRITQLTFDERFGLDEPEDDICKYDFVEVEPSPGSVYL 120
 QY 121 GRMCGSGTVPGKQTSKGNHIRIRFVSDSEYFSPGFCIHYSIIMPOVETTSVLPSPSS 180
 DB 121 GRMCGSGTVPGKQTSKGNHIRIRFVSDSEYFSPGFCIHYSIIMPOVETTSVLPSPSS 180
 QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVDDSLYKPTWOLGKAFVGRKSKVNVNL 240
 DB 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVDDSLYKPTWOLGKAFVGRKSKVNVNL 240
 QY 241 LKEEVKLYSCFPRNFVSISREELKRTDTLFWPGCLLVKRCGGACCLNNECCQCVPRK 300
 DB 241 LKEEVKLYSCFPRNFVSISREELKRTDTLFWPGCLLVKRCGGACCLNNECCQCVPRK 300
 QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345
 DB 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345

RESULT 12

AAB44322 standard; Protein; 345 AA.

XX AAB44322;

DT 08-FEB-2001 (first entry)

DE Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.

KM Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
 expressed sequence tag; detection; cancer.

OS Homo sapiens.

PN WO200053756-A2.

PD 14-SEP-2000.

PF 18-FEB-2000; 2000WO-US04341.

PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 29-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.

XX (GENTH) GEMENTECH INC.

PI Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Fillauroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kijavini JJ, Kuo SS, Napier MA, Pan J, Peoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT.

XX WPI: 2000-611443/58.

DR N-PSDB: AAC78582.

XX Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities.

XX Claim 12: Fig 207: 636pp: English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC79987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.

XX Sequence 345 AA:

Query Match 90.2%; Score 1667; DB 21; Length 345;

Best Local Similarity 87.0%; Pred. No. 3.2e-163;

Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGORTGTRAESNLSSKQLQSSDKQNGVODPRHERVTTSGNGSIHS 60
 DB 1 MSLLFGLLLTSLAGORGTQAESNLSSKFQSSNKEQNGVODPOHERITIVSTNGSIHS 60
 QY 61 PKRPHTYPRNNMVLWRLVAVDENVRITQLTFDERFGLDEPEDDICKYDFVEVEPSPGSVYL 120
 DB 61 PKRPHTYPRNNMVLWRLVAVDENVRITQLTFDERFGLDEPEDDICKYDFVEVEPSPGSVYL 120
 QY 121 GRMCGSGTVPGKQTSKGNHIRIRFVSDSEYFSPGFCIHYSIIMPOVETTSVLPSPSS 180
 DB 121 GRMCGSGTVPGKQTSKGNHIRIRFVSDSEYFSPGFCIHYSIIMPOVETTSVLPSPSS 180
 QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVDDSLYKPTWOLGKAFVGRKSKVNVNL 240
 DB 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVDDSLYKPTWOLGKAFVGRKSKVNVNL 240
 QY 241 LKEEVKLYSCFPRNFVSISREELKRTDTLFWPGCLLVKRCGGACCLNNECCQCVPRK 300
 DB 241 LKEEVKLYSCFPRNFVSISREELKRTDTLFWPGCLLVKRCGGACCLNNECCQCVPRK 300
 QY 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345
 DB 301 VTKKYHEVLQLRPKTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345

RESULT 13

AAB10633 standard; Protein; 345 AA.

XX AAB10633;

XX	19-JAN-2001	(first entry)	
DT			
XX			
DE			
XX			
XX			
KW	Human RACE generated VEGF-X protein.		
KW	VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic;		
KW	antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;		
KW	angiogenesis regulator; vascularization regulator; cancer; psoriasis;		
KW	rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;		
KW	tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;		
KW	venous sore; diabetic ulcer; burns; skin graft growth.		
XX			
OS	Homo sapiens.		
PN	WO200037641-A2.		
XX			
PD	29-JUN-2000.		
XX			
PF	21-DEC-1999; 99WO-US30503.		
XX			
PR	22-DEC-1998; 98GB-0028377.		
PR	18-MAR-1999; 99US-0124967.		
XX			
PR	08-NOV-1999; 99US-0164131.		
XX			
PA	(JANC) JANSSEN PHARM NV.		
PI	Gordon RD, Sprengel JF, Yon JR, Dijkmans JFH, Goslowska A;		
PI	Dhanaraj SM, Xu J;		
XX			
DR	WPI; 2000-442669/38.		
DR	N-PSDB; AAA71951.		
XX			
PT	New vascular endothelial growth factor protein, useful for treating or		
PT	preventing diseases associated with inappropriate angiogenesis activity		
XX	such as cancer, rheumatoid arthritis, psoriasis and wounds		
XX			
PS	Disclosure; Fig 6; 127pp; English.		
XX			
CC	This invention describes a novel vascular endothelial growth factor-X		
CC	(VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has		
CC	vulnerary, cyostatic, antirheumatic, antiarthritic, antipsoriatic and		
CC	antidiabetic activity and acts as an angiogenesis and vascularization		
CC	regulator. An antisense molecule of the invention is useful for treating		
CC	or preventing cancer, rheumatoid arthritis, psoriasis and diabetic		
CC	retinopathy by inhibiting angiogenic activity or inappropriate		
CC	vascularization including formation and proliferation of new blood		
CC	vessels, growth and development of tissues, tissue regeneration and organ		
CC	and tissue repair in a subject. The products of the invention are useful		
CC	for preparing medicaments for treating wounds such as dermal ulcers,		
CC	pressure sores, venous sores, diabetic ulcers and burns and to promote		
CC	skin graft growth, tissue repair, proliferation of new blood vessels,		
CC	tissue regeneration and organ repair by promoting angiogenic activity or		
CC	vascularization. This sequence represents the RACE generated human VEGF-X		
CC	protein described in the method of the invention.		
XX			
SO	Sequence 345 AA:		
	Query Match 90.2%; Score 1667; DB 21; Length 345;		
	Best Local Similarity 87.0%; Pred. No. 3,2e-163;		
	Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0		
OY	1 MLLGLLTLTSLACORTPTAESNLSSKLTLSLSDKEQGVDPDRHRRVYTTISGNSIHS 60		
DB	1 MLLGLLTLTSLACORTPTAESNLSSKLTLSLSDKEQGVDPDRHRRVYTTISGNSIHS 60		
OY	1 MLLGLLTLTSLACORTPTAESNLSSKLTLSLSDKEQGVDPDRHRRVYTTISGNSIHS 60		
DB	1 MLLGLLTLTSLACORTPTAESNLSSKLTLSLSDKEQGVDPDRHRRVYTTISGNSIHS 60		
OY	61 PRPHPTYPNNWLVWRLVAVDENVRIQLTFDERFGLEDEDDICKYDFVEVEEPPSGSVL 120		
DB	61 PRPHPTYPNNWLVWRLVAVDENVRIQLTFDERFGLEDEDDICKYDFVEVEEPPSGSVL 120		
OY	121 GWMCGSGTYPGKOTSGNIIIRFVSDYDFPSPGCGICHTYTIMPOVTEFTSSVLPSPS 180		
DB	121 GWMCGSGTYPGKOTSGNIIIRFVSDYDFPSPGCGICHTYTIMPOVTEFTSSVLPSPS 180		
OY	121 GWMCGSGTYPGKOTSGNIIIRFVSDYDFPSPGCGICHTYTIMPOVTEFTSSVLPSPS 180		
DB	121 GWMCGSGTYPGKOTSGNIIIRFVSDYDFPSPGCGICHTYTIMPOVTEFTSSVLPSPS 180		

Oy	181	LSLILNNAAVASTPEELIRYLEPRRMOVDLSLKPPMOLLGFAFLVGKSKSVNLN	240
Dd	181	LPLDLNLNATTAASSTEDLLRYLEPERKWOLDLEDLYRPWOLLGAFVGRKSRAVDNLN	240
Oy	241	LKEEKKLVSCPTPNFVSISIREELKRDTDTTFWPCCLLVKRCGGNCACCLHNECCOCPBRK	300
Dd	241	LTEEVRLTSCPTPNFVSISIREELKRDTDTTFWPCCLLVKRCGGNCACCLHNECCOCPYSK	300
Oy	301	VTKKYHEVLQLRPKTVGVKLHKSLTDVALHHNEECDCVCRGNAAG	345
Dd	301	VTKKYHEVLQLRPKTVGVRLHKSLTDVALHHNEECDCVCRGSTGG	345
RESULT 14			
RAB10635	ID	AAB10635 standard; Protein; 345 AA.	
XX	AC	AAB10635;	
XX	DT	19-JAN-2001 (first entry)	
XX	DE	Human VEGF-X protein #1 isolated from clones 4 and 7.	
XX	KM	VEGF-X: vascular endothelial growth factor; human; vlneryary; cytostatic;	
KM	KM	antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;	
KM	KM	angiogenesis regulator; vascularization regulator; cancer; psoriasis;	
KM	KM	rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;	
KM	KM	tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;	
KM	KM	venous sore; diabetic ulcer; burns; skin graft growth.	
XX	OS	Homo sapiens.	
XX	PN	WO200037641-A2.	
XX	PD	29-JUN-2000.	
Pf	21-DEC-1999;	99NO-US030503.	
XX	PR	22-DEC-1998; 98GB-0028377.	
PR	18-MAR-1999;	99US-0124967.	
PR	08-NOV-1999;	99US-0164131.	
XX	PA	(JANC) JANSSEN PHARM NV.	
XX	PI	Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJJH, Gosiowska A;	
PI	PI	Dhanaraj SN, Xu T;	
XX	DR	WPI: 2000-442669/38.	
DR	N-PSDB:	AAA71955.	
XX	PT	New vascular endothelial growth factor protein, useful for treating or	
PT	PT	preventing diseases associated with inappropriate angiogenesis actively	
XX	PS	such as cancer, rheumatoid arthritis, psoriasis and wounds -	
XX	PS	Disclosure; Fig 9, 12/pp: English.	
XX	XX	This invention describes a novel vascular endothelial growth factor X	
CC	CC	(VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has	
CC	CC	vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and	
CC	CC	antidiabetic activity and acts as an angiogenesis and vascularization	
CC	CC	regulator. An antisense molecule of the invention is useful for treating	
CC	CC	or preventing cancer, rheumatoid arthritis, psoriasis and diabetic	
CC	CC	retinopathy by inhibiting angiogenic activity or inappropriate	
CC	CC	vascularization including formation and proliferation of new blood	
CC	CC	vessels, growth and development of tissues, tissue regeneration and organ	
CC	CC	and tissue repair in a subject. The products of the invention are useful	
CC	CC	for preparing medicaments for treating wounds such as dermal ulcers,	
CC	CC	pressure sores, venous sores, diabetic ulcers and burns and to promote	
CC	CC	skin graft growth, tissue repair, proliferation of new blood vessels,	
CC	CC	tissue regeneration and organ repair by promoting angiogenic activity or	
CC	CC	vascularization. This sequence represents the human VEGF-X protein	
XX	XX	isolated from clones 4 and 7 described in the method of the invention.	

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GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 09:08:16 ; Search time 26.5 Seconds

(without alignments)
1043.199 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLLTLTSALAGQRTGT.....DVALEHHECDCCVCRGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1848	100.0	345	US-09-852-209A-7	Sequence 7, Appl1
2	1848	100.0	345	US-10-139-583-43	Sequence 43, Appl1
3	1848	100.0	345	US-09-823-033-4	Sequence 4, Appl1
4	1848	100.0	345	US-09-818-943-2	Sequence 2, Appl1
5	1667	90.2	345	US-09-978-295A-488	Sequence 488, App
6	1667	90.2	345	US-09-978-697-488	Sequence 488, App
7	1667	90.2	345	US-09-978-192A-488	Sequence 488, App
8	1667	90.2	345	US-10-139-583-2	Sequence 488, App
9	1667	90.2	345	US-09-999-832A-488	Sequence 488, App
10	1667	90.2	345	US-09-978-189-488	Sequence 488, App
11	1667	90.2	345	US-10-028-072-286	Sequence 286, App
12	1667	90.2	345	US-10-121-049-286	Sequence 286, App
13	1667	90.2	345	US-10-123-904-286	Sequence 286, App
14	1667	90.2	345	US-10-140-470-286	Sequence 286, App
15	1667	90.2	345	US-09-796-753-6	Sequence 6, Appl1
16	1667	90.2	345	US-10-175-746-286	Sequence 286, App
17	1667	90.2	345	US-10-176-918-286	Sequence 286, App
18	1667	90.2	345	US-10-176-921-286	Sequence 286, App
19	1667	90.2	345	US-10-103-197-4	Sequence 4, Appl1

20	1667	90.2	345	US-10-137-865-286	Sequence 286, App
21	1667	90.2	345	US-10-140-474-286	Sequence 286, App
22	1667	90.2	345	US-10-142-431-286	Sequence 286, App
23	1667	90.2	345	US-10-143-114-286	Sequence 286, App
24	1667	90.2	345	US-10-140-002-286	Sequence 286, App
25	1667	90.2	345	US-09-978-608A-488	Sequence 488, App
26	1667	90.2	345	US-10-142-419-286	Sequence 286, App
27	1667	90.2	345	US-09-978-191A-488	Sequence 488, App
28	1667	90.2	345	US-09-978-403A-488	Sequence 488, App
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31	1667	90.2	345	US-10-017-081A-488	Sequence 488, App
32	1667	90.2	345	US-10-123-263-286	Sequence 286, App
33	1667	90.2	345	US-10-142-423-286	Sequence 286, App
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35	1667	90.2	345	US-09-981-915A-488	Sequence 488, App
36	1667	90.2	345	US-09-999-833A-488	Sequence 488, App
37	1667	90.2	345	US-10-121-050-286	Sequence 286, App
38	1667	90.2	345	US-10-141-755-286	Sequence 286, App
39	1667	90.2	345	US-10-167-749-488	Sequence 488, App
40	1667	90.2	345	US-09-918-585A-488	Sequence 488, App
41	1667	90.2	345	US-10-143-032-286	Sequence 286, App
42	1667	90.2	345	US-09-978-423A-488	Sequence 488, App
43	1667	90.2	345	US-10-013-921A-488	Sequence 488, App
44	1667	90.2	345	US-10-123-108-286	Sequence 286, App
45	1667	90.2	345	US-10-123-236-286	Sequence 286, App

ALIGNMENTS

RESULT 1
US-09-852-209A-7
Sequence 7, Application US/09852209A
Patent No. US20020164687A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PORTEN, Annica
APPLICANT: ULTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: BETHSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al 1-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 345
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-852-209A-7
Query Match 100.0% Score 1848: DB 9: Length 345:
Best Local Similarity 100.0% Pred. NO. 1.5e-155:
Matches 345: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 MLLGLLTLTSALAGQRTGTAAESNLISKLQLSDEKQGVQDPFRHRRVVTISGNCSHS 60

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Db      1 MLLGLLLLSALAGORTGTRAESNLSKQLQSSDKQONCVOPRHRVVTISGNGSIHS 60
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Db      61 PKPHTYPRMVMVWRLVAVDENVRIQLTDERGLEDPEDDICKYFVEVEEPSDGSVL 120
OY      121 GRMGSGTVPGKOTSKGNHIRIFVSDPEPSPGFCIHYSIIMPOVTEETSPSVLPSS 180
Db      121 GRMGSGTVPGKOTSKGNHIRIFVSDPEPSPGFCIHYSIIMPOVTEETSPSVLPSS 180
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Db      181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTMQLLGAFLYKSKSVVNL 240
OY      241 LKEEVKLYSCTPRNFVSISIEELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQVPRK 300
Db      241 LKEEVKLYSCTPRNFVSISIEELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQVPRK 300
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Db      301 VTKKHYEVLQLRPKTGKGLHKSITDVALEHHEBCDCVCGNAG 345

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RESULT 2

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US-10-139-583-43
; Sequence 43, Application US/10139583
; Patent No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVECF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-139-583-43

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Query Match 100.0%; Score 1848; DB 9; Length 345;

Best Local Similarity 100.0%; Pred. No. 1.5e-155;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61 PKPHTYPRMVMVWRLVAVDENVRIQLTDERGLEDPEDDICKYFVEVEEPSDGSVL 120
OY      121 GRMGSGTVPGKOTSKGNHIRIFVSDPEPSPGFCIHYSIIMPOVTEETSPSVLPSS 180
Db      121 GRMGSGTVPGKOTSKGNHIRIFVSDPEPSPGFCIHYSIIMPOVTEETSPSVLPSS 180
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Db      181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTMQLLGAFLYKSKSVVNL 240
OY      241 LKEEVKLYSCTPRNFVSISIEELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQVPRK 300
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RESULT 3

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US-09-823-033-4
; Sequence 4, Application US/09823033
; Patent No. US20020004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-823-033-4

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Query Match 100.0%; Score 1848; DB 10; Length 345;

Best Local Similarity 100.0%; Pred. No. 1.5e-155;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      121 GRMGSGTVPGKOTSKGNHIRIFVSDPEPSPGFCIHYSIIMPOVTEETSPSVLPSS 180
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Db      181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTMQLLGAFLYKSKSVVNL 240
OY      241 LKEEVKLYSCTPRNFVSISIEELKRTDTIFWPGCLVYKRCGNCACCLHNCNECQVPRK 300
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RESULT 4

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US-09-818-943-2
; Sequence 2, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: Li, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: Li, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWT
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7

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SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 345
TYPE: prt
ORGANISM: Murinae gen. sp.
US-09-818-943-2

Query Match 100.0%; Score 1848; DB 10; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.5e-155;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLLGLLLTSLAAGQRTGTRAESNLSSKQLQSDKEQNGVODPRHRYVITSGNSIHS 60
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DB 61 PKPHTYPRNMYLVAVYDENVRQLTFDERFGLEDEDEDICKYDFEVEEPPSGSVL 120
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RESULT 5
US-09-978-295A-488
Sequence 488, Application US/09978295A
Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desmoyers, Luc
APPLICANT: Eaton Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630FIC11
CURRENT APPLICATION NUMBER: US/09/978, 295A
CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/077632
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
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PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
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PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
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PRIOR FILING DATE: 1998-04-08
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203

;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081229
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081955
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;; PRIOR APPLICATION NUMBER: 60/081817
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 1, 6e-139;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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QY 121 GRWGSGTVPKQTSKGNHRIREFVSDPEPSEPGFCHISIMPOVETTSVLPSS 180
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QY 181 LSLDLLNNAVAFSTLEELIRYLEPDRQVLDLSKPYTQLLGAKFLYGGKSKVYNLNL 240
181 LPDLLNNAITAFSTLEELIRYLEPDRQVLDLSKPYTQLLGAKFLYGGKSKVYNLNL 240
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QY 241 LKEEVKLYSTPRNFVSSTIEELKRTDTITWPGCLLYKRCGMCACCLHNCNCQCVPRK 300
241 LKEEVRLYSTPRNFVSSTIEELKRTDTITWPGCLLYKRCGMCACCLHNCNCQCVPSK 300
Db
QY 301 VTKKHYEVLQLRPKTGKGLKSLTDVALEHHECDVCVCGNAGG 345
301 VTKKHYEVLQLRPKTGKGLKSLTDVALEHHECDVCVCGNAGG 345
Db
301 VTKKHYEVLQLRPKTGKGLKSLTDVALEHHECDVCVCGNAGG 345

RESULT 6
US-09-978-697-488
; Sequence 488, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvarolf, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austen L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kjaavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT FILING DATE: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Query Match      90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 1.6e-139;
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Db 121 GRMGSGTVGKQTSKGNHTRFVSDYPPSPFCIHSTIIMPOVETTSVLPSS 180
QY 181 LSLDLNNAVTAESTLEELIRYLEPPRMVYDLDSLKKPTWQLLGAFLYKSKSVNL 240
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Db 241 LKEEVKLYSTPRNFVSSTIEELKRTDTITWPGCLLVKRCGNCACCLHNCNECCVPRK 300
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Db 301 VTKKYEVLQLRKPTGYKGLKSLTDVLEHHECCDVCVCGNAG. 345

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RESULT 7
US-09-978-192A-488
Sequence 488, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon

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: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
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: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
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: APPLICANT: Kijavitt, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630P1C9
: CURRENT APPLICATION NUMBER: US/09/978,192A
: PRIOR FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: 09/918585
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44 PRIOR FILING DATE: 1998-05-15
45 PRIOR APPLICATION NUMBER: 60/085697

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[illegible]

RESULT 8
US-10-139-583-2
Sequence 2, Application US/10139583
Patent No. US20020177193A1
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/10/139,583
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/457,066
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-10-139-583-2

Query Match 90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 1,6e-119;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

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DB 61 PRPHPTPRMTVLVWRLVAEENWVQLTFDEREGLEDPEDDICKYDFVEVEEPPSDSVL 120
QY 121 GRWGSGTIVGKQTSKGNHRIKRVSDYFPPSEFGCIHNSIIMPQVTEITTSVPLPSS 180
DB 121 GRWGSGTIVGKQTSKGNHRIKRVSDYFPPSEFGCIHNSIIMPQVTEITTSVPLPSS 180
QY 181 LSLDLNNATAFSTLEELRYLEPPDMOYDLDSLYKPTWQLGKAPLYGKSKVVDNL 240
DB 181 LSLDLNNATAFSTLEELRYLEPPDMOYDLDSLYKPTWQLGKAPLYGKSKVVDNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQLRPTGYKGLKSLTDVALLEHNECCDCVCSNAGG 345
DB 301 VTKKYHEVLQLRPTGYKGLKSLTDVALLEHNECCDCVCSNAGG 345

RESULT 9
US-09-999-832A-488
Sequence 486, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Hong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavyn, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
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PRIOR FILING DATE: 2001-07-30
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43	PRIOR FILING DATE: 1998-05-15	
44	PRIOR APPLICATION NUMBER: 60/0856597	

Query Match	90.2%	Score 1667;	DB 9;	length 345;
Best Local Similarity	87.0%;	Pred. No. 1.6e-139;		
Matches 300;	Conservative 27;	Mismatches 18;	Indels 0;	Gaps 0;

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Dd	1	MSLGLLELITLALGQKQIOAESNLSKIOFSSNKQONQVOPQHRITITVINGSIHS	60
QY	61	PKPFPYPRNNVLWVRIVAVDENRIO,LTDERGLEDPEDDICKQYFVEEPPSDSVL	120
Dd	61	PRFPHTYPRNVVLWVRIVAVDENWIO,LTDERGLEDPEDDICKQYFVEEPPSDSTIL	120
QY	121	GRMGSGTVPKQOTSKGNIHRI,RPVSDVEYPPSEFGCIHYSIIMPQYETITSESVLPSS	180
Dd	121	GRMGSGTVPKQOTSKGNOI,RI,RPVSDVEYPPSEFGCIHINIMYPOQTEAVSPSVLPSSA	180
QY	181	LSDDLNNAVTAEESTLEBLI,RYLEBDRQYDLOS,LYKFTMQLGKAFL,YGKSKRVNML	240
Dd	181	LPDLNNAVTAEESTLEBLI,RYLEBDRQYDLEDT,LYPQMQLGKAFLVFGKSKRVVDLNL	240
QY	241	LKEEVKILYSCPRNFVS,SI,REELKRTDTI,IMPGLLYKRCGGACACILHNCNECOCYPRK	300
Dd	241	LTEEVRLYSCPRNFVS,SI,REELKRTDTI,IMPGLLYKRCGGACACILHNCNECOCYPSK	300
QY	301	VTKKYUHEYLQRPKTGYKGLHKS,LTVDALENHNECOCVGRGNNG	345
Dd	301	VTKKYUHEYLQRPKTGYKGLHKS,LTVDALENHNECOCVGRGNNG	345

RESULT 10
US-09-978-189-488
; Sequence 488, Application US/09978189

Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1997-10-24	PRIOR APPLICATION NUMBER: 60/063327
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Db      301 VTAKKHEVQLRPRKTGVRLHKSLLDVALLEHHBECDCVCRGSTGG   345

RESULT 14
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; Publication No. US2003002231A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvarioff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zhenlu
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C160
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; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
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; SEQ ID NO 286
; LENGTH: 345
; TYPE: PRP
; ORGANISM: Homo Sapien
US-10-140-470-286

Query Match          90.2%; Score 1667; Dn 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 1,6e-139;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

OY      1 MLILGLLITSLAAGQRTGTAESENLSKTLQSSDKEQNGVODPRHERVYTISGNSIHS   60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MSFLGILLITSLALAQROCTQAESNLSKFQSSNKENGVOQPHERITIVTSGNSIHS   60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      61 PKFPHTYPRNMVLWRLVAVDENVNIQLTFDRFGLEGDEPDICKDYVEVEEPPSDGSYL   120
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 PREPHTYPRAVTLVWRLVAVEENVMVLIOLFDERFGLDEPDICKDYFEVEEEPSDGLTL   120
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      121 GWCGSGTVPGKQTSGKNHIRIRFYSDSEFPSPGFCIHYSIIIMPOVETTSRPSVLPESS   180
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 GRMGCSGYIPGKQJOKSQRNDIRIRFVSDEFEPSPGFCIHYNIMQPFTEANSPSVLPESA   180
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      181 LSLLDLNNAVTAFTLEEELIRYLEBDNRQVDDSDSYKPTMQLLGKAFTLYGKKSKYVNLT.   240
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 LPDLLDNNAITAFSTLEDLIRYLEPERMQLDDEDLYLRPTMQLGKAFAFGKRSRVVDNL.   240
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      241 LKEEKVLYSCIPRNRSVSIREDLKRTDTIIFWGCLLYVRGCGNCACCLHNCECCVPRK   300
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      241 LTREERLYSCIPRNRSVSIREDLKRTDTIIFWGCLLYVRGCGNCACCLHNCECCVPESK   300
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      301 VTKKHEVQLRPKTGVGKGLHKSLLDVALLEHHBECDCVCRGNAGG   345
        |||||||.....:|||||||.....:|||||||.....:|||||||.....:
Db      301 VTAKKHEVQLRPRKTGVRLHKSLLDVALLEHHBECDCVCRGSTGG   345
        |||||||.....:|||||||.....:|||||||.....:|||||||.....:

RESULT 15
US-09-796-753-6
Sequence 6, Application US/09796753
Publication No. US2003002798A1

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: GENERAL INFORMATION:
: APPLICANT : McCarthy, Sean A.
: TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
: FILE REFERENCE: 7853-227-999
: CURRENT APPLICATION NUMBER: US/09/796,753
: PRIOR FILING DATE: 2001-03-01
: PRIOR APPLICATION NUMBER: 09/183,175
: PRIOR FILING DATE: 1998-10-30
: PRIOR APPLICATION NUMBER: 09/223,094
: PRIOR FILING DATE: 1998-12-30
: PRIOR APPLICATION NUMBER: 09/223,546
: PRIOR FILING DATE: 1998-12-30
: PRIOR APPLICATION NUMBER: 09/224,246
: PRIOR FILING DATE: 1998-12-30
: PRIOR APPLICATION NUMBER: 09/259,388
: PRIOR FILING DATE: 1999-02-26
: PRIOR APPLICATION NUMBER: 60/122,458
: PRIOR FILING DATE: 1999-03-01
: PRIOR APPLICATION NUMBER: 09/312,359
: PRIOR FILING DATE: 1999-05-14
: PRIOR APPLICATION NUMBER: 09/336,536
: PRIOR FILING DATE: 1999-06-18
: PRIOR APPLICATION NUMBER: 09/342,687
: PRIOR FILING DATE: 1999-06-29
: PRIOR APPLICATION NUMBER: 09/345,464
: PRIOR FILING DATE: 1999-06-30
: PRIOR APPLICATION NUMBER: 09/365,164
: PRIOR FILING DATE: 1999-07-30
: PRIOR APPLICATION NUMBER: 09/399,723
: PRIOR FILING DATE: 1999-09-20
: PRIOR APPLICATION NUMBER: 09/409,634
: PRIOR FILING DATE: 1999-09-30
: PRIOR APPLICATION NUMBER: 09/471,179
: PRIOR FILING DATE: 1999-12-23
: PRIOR APPLICATION NUMBER: 09/474,071
: PRIOR FILING DATE: 1999-12-29
: PRIOR APPLICATION NUMBER: 09/474,072
: PRIOR FILING DATE: 1999-12-29
: PRIOR APPLICATION NUMBER: 09/514,010
: PRIOR FILING DATE: 2000-02-25
: PRIOR APPLICATION NUMBER: 09/516,745
: PRIOR FILING DATE: 2000-03-01
: PRIOR APPLICATION NUMBER: 09/572,002
: PRIOR FILING DATE: 2000-05-14
: PRIOR APPLICATION NUMBER: 09/597,993
: PRIOR FILING DATE: 2000-06-19
: PRIOR APPLICATION NUMBER: 09/599,596
: PRIOR FILING DATE: 2000-06-22
: PRIOR APPLICATION NUMBER: 09/630,334
: PRIOR FILING DATE: 2000-07-31
: PRIOR APPLICATION NUMBER: 09/606,565
: PRIOR FILING DATE: 2000-06-29
: PRIOR APPLICATION NUMBER: 09/606,317
: PRIOR FILING DATE: 2000-06-29
: PRIOR APPLICATION NUMBER: 09/665,666
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: 09/677,751
: PRIOR FILING DATE: 2000-09-30
: NUMBER OF SEQ ID NOS: 162
: SEQ ID NO 6
: LENGTH: 345
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-796-753-6

Query Match          90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 1,6e-13;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

OY      1  MLTGLILLTSLAAGRGTRAEASLSTKLOLSDPKEDONGVODPHERVITSGNGSIHS 60
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  MSRLRLLLTSLAAGRGTRAEASLSTKLOLSDPKEDONGVODPHERITVSTNGSIHS 60

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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:03:41 ; Search time 55 Seconds
(without alignments)
1292.477 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLLLTSLALGQRTGT.....DVALHHEBCDCVCRGNAGG 345

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	345	11	Q90Y71 mus musculus
2	1819	98.4	345	11	Q9JHV8 mus musculus
3	1801	97.5	345	11	Q9EQX6 rat mus musculus
4	1667	90.2	345	11	Q9UL22 rat mus musculus
5	1664	90.0	345	11	Q9NRA1 rat mus musculus
6	1552	84.0	345	13	Q91946 gallus gallus
7	754	40.8	370	11	Q9EQT1 rat mus musculus
8	752	40.7	370	4	Q9G2P0 homo sapien
9	750.5	40.6	364	4	Q9BHV5 homo sapien
10	746.5	40.4	370	11	Q92517 mus musculus
11	660	35.7	290	11	Q9D1L8 mus musculus
12	201	10.9	923	13	Q8GFX6 brachydanio
13	192.5	10.4	691	13	Q57658 gallus gallus
14	192	10.4	34	11	Q99JH4 mus musculus
15	191	10.3	977	13	Q91925 xenopus lae
16	186	10.1	735	13	Q57381 xenopus lae

17	185	10.0	926	4	Q9U000	Q9U000 homo sapien
18	185	10.0	1015	4	Q9Y6L7	Q9Y6L7 homo sapien
19	183	9.9	1012	11	Q9WVM6	Q9WVM6 mus musculus
20	181	9.8	241	11	Q9Z135	Q9Z135 rat mus musculus
21	176	9.5	609	4	Q96190	Q96190 homo sapien
22	176	9.5	644	4	Q961H5	Q961H5 homo sapien
23	176	9.5	704	4	Q9H2E1	Q9H2E1 homo sapien
24	174.5	9.4	3623	4	Q60494	Q60494 homo sapien
25	169	9.1	1008	13	Q9DER7	Q9DER7 gallus gallus
26	168	9.1	921	11	Q90X38	Q90X38 rat mus musculus
27	165	8.9	1013	11	Q62381	Q62381 mus musculus
28	165	8.9	1019	13	Q57382	Q57382 xenopus lae
29	162	8.8	1013	4	Q43897	Q43897 homo sapien
30	162	8.8	1013	4	Q9N0S4	Q9N0S4 homo sapien
31	161.5	8.7	919	13	Q8UVR0	Q8UVR0 gallus gallus
32	161.5	8.7	936	13	Q8UV09	Q8UV09 gallus gallus
33	160	8.7	3623	11	Q70244	Q70244 rat mus musculus
34	158.5	8.6	926	11	Q802Y7	Q802Y7 mus musculus
35	158	8.5	3620	6	Q9TU53	Q9TU53 canis fam1
36	157	8.5	276	4	Q9BRH3	Q9BRH3 homo sapien
37	157	8.5	415	4	Q9UKZ9	Q9UKZ9 homo sapien
38	155.5	8.4	555	4	Q9H2E2	Q9H2E2 homo sapien
39	155.5	8.4	901	4	Q9H2E4	Q9H2E4 homo sapien
40	155.5	8.4	901	4	Q9H2D5	Q9H2D5 homo sapien
41	155.5	8.4	906	4	Q9H2E3	Q9H2E3 homo sapien
42	155.5	8.4	906	4	Q9H2D4	Q9H2D4 homo sapien
43	150.5	8.1	686	13	Q9DGC2	Q9DGC2 cyprinus ca
44	149	8.1	212	11	Q09020	Q09020 rat mus musculus
45	149	8.1	701	11	Q9JJS9	Q9JJS9 rat mus musculus

ALIGNMENTS

RESULT 1
ID Q90Y71 PRELIMINARY: PRT; 345 AA.
AC Q90Y71;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Fallottein (Platelet-derived growth factor C).
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RP TISSUE-Ovary;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RT "cDNA cloning of fallottein from mouse ovary."
RN Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
RA Gilbertson D., West J., O'Hara P.J.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that
RT binds to PDGF alpha receptor."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF117608; AAF22516.1; -;
DR EMBL: AF266467; AAK58566.1; -;
DR MGD: MGI:1859631; Pd9fc.
DR InterPro: IPR000859; CUB_domain.
DR Pfam: PF00431; CUB_1.
DR Pfam: PF00341; PDGF_1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.

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SQ SEQUENCE 345 AA: 38741 MW: 3A58A1F701B84EA2 CRC64;
Query Match 100.0%; Score 1848; DB 11; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.4e-162;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKQONGVQDPRHRVYVITISNGSIHS 60
DB 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKQONGVQDPRHRVYVITISNGSIHS 60
QY 61 PKPHTYPRNMVLYWRLVAADENVRIQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKPHTYPRNMVLYWRLVAADENVRIQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
QY 61 PKPHTYPRNMVLYWRLVAADENVRIQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKPHTYPRNMVLYWRLVAADENVRIQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
DB 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
QY 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
DB 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMAYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240
DB 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMAYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240
QY 241 LKEEVKLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALEHHECCDCVCRGNAG 345
DB 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALEHHECCDCVCRGNAG 345

RESULT 2
ID Q9JHV8 PRELIMINARY; PRT: 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Platelet-derived growth factor C.
GN PDGFC.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS-WEBSTER/NIH;
RX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during
RT organogenesis.";
RL Mech. Dev. 96:209-213(2000).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF286725; AAF91483.1; -.
DR MGD: MGI:1859631; PdGfc.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00431; CUB: 1.
DR SMART: SM00042; CUB: 1.
DR SMART: SM00141; PDGF: 1.
DR PROSITE: PS01180; CUB: 1.
DR PROSITE: PS50278; PDGF_2: 1.
DR PROSITE: PS50278; PDGF_2: 1.
SQ SEQUENCE 345 AA: 38886 MW: FA1486BEDD362F8 CRC64;

Query Match 98.4%; Score 1819; DB 11; Length 345;
Best Local Similarity 98.8%; Pred. No. 6.9e-160;
Matches 341; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKQONGVQDPRHRVYVITISNGSIHS 60
DB 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKQONGVQDPRHRVYVITISNGSIHS 60
QY 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKQONGVQDPRHRVYVITISNGSIHS 60
DB 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKQONGVQDPRHRVYVITISNGSIHS 60
QY 61 PKPHTYPRNMVLYWRLVAADENVRIQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120

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DB 61 PKPHTYPRNMVLYWRLVAADENVRIQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
DB 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
QY 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
DB 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMAYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240
DB 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMAYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240
QY 241 LKEEVKLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGCACCLHNCNECQVPRK 300
DB 241 LKEEVKLYSCTPRNFVSIREELKRTDTIFWPGLLVKRCGCACCLHNCNECQVPRK 300
QY 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALEHHECCDCVCRGNAG 345
DB 301 VTKKYHEVLQLRPKTVGKGLHKSITDVALEHHECCDCVCRGNAG 345

RESULT 3
ID Q9EOX6 PRELIMINARY; PRT: 345 AA.
AC Q9EOX6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Spinal cord-derived growth factor.
GN RSCDGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=KIDNEY;
RX MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ui-Tel K., Imaki Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
RT SCDF/PDGF-C/fallopain.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AB033830; BAB19969.1; -.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00431; CUB: 1.
DR Pfam: PF00341; PDGF: 1.
DR SMART: SM00042; CUB: 1.
DR SMART: SM00141; PDGF: 1.
DR PROSITE: PS01180; CUB: 1.
DR PROSITE: PS50278; PDGF_2: 1.
DR PROSITE: PS50278; PDGF_2: 1.
SQ SEQUENCE 345 AA: 38734 MW: F296DA6E9B765D10 CRC64;

Query Match 97.5%; Score 1801; DB 11; Length 345;
Best Local Similarity 96.8%; Pred. No. 3.2e-158;
Matches 334; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKQONGVQDPRHRVYVITISNGSIHS 60
DB 1 MLLGLLLLSALAGORTGTRAESNLSSKQLQSSDKQONGVQDPRHRVYVITISNGSIHS 60
QY 61 PKPHTYPRNMVLYWRLVAADENVRIQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKPHTYPRNMVLYWRLVAADENVRIQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
QY 61 PKPHTYPRNMVLYWRLVAADENVRIQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKPHTYPRNMVLYWRLVAADENVRIQLTFDERGLEDPEDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
DB 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
QY 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
DB 121 GRMGSGTVPKQTSKGNHRIREFVSDYEPSEPGFCIHYSIIMPQYETTTSPSVLPSS 180
QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMAYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240
DB 181 LSLDLNNAVTAFTSTLEELIRYLEPDRMAYDLSLYKPTMQLGKAPLYGKRSKVNLNL 240

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Oy	241	LKEEYKATSCPPRNFSVISIRELKRTPDIIPFGCLYKRCGGNACCLHNCNECCYPRK	300
Db	241	LKEEYKATSCPPRNFSVISIRELKRTPDIIPFGCLYKRCGGNACCLHNCNECCYPRK	300
Oy	301	VTKKYHNEVLDLRPKTGVKGLKSLTDVALENNEECDCVCRRNMG	345
Db	301	VTKKYHNEVLDLRPKTGVKGLKSLTDVALENNEECDCVCRRNMG	345

RESULT 4

ID	Q9UL22	PRELIMINARY;	PRT;	345	AA
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DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Secretary growth factor-like protein FALLOTIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).
DE SOURCE: de novo

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS.
RA Tsai Y.J., Lee R.K.K., Lin S.P.,
RT "Pallonein, a novel growth factor like gene identified in human
UTERUS.",
RL submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE-20317014; PubMed-10858496;
RA Hamada T., Ut-Tel K., Miyata I.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
TL member of the PDGF/VbGF family."; FEBS Lett. 475:97-102(2000).

RP SEQUENCE FROM N.A.
RX MEDLINE/21347863; PubMed/11297552;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Holstrand P.D., Gao Z., Shomaker K., Bukowski T.R., Moore M.,
RA Heidtman A.L., Humes J.M., Palmer T.E., Hart C.E.).
RT "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That
RT Binds to PDGF alpha and beta Receptor.";
CC J. Biol. Chem. 276:27406-27414(2001).
-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

DR EMBL: AF031434; AAC00042.1; -
DR EMBL: AB033831; BAB03266.1; -
DR EMBL: AF260738; AAK51637.1; -
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00341; PDGF; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC644

Query Match	90.23;	Score 1657;	DB 4;	Length 345;
Best Local Similarity	87.08;	Pred. No. 7.8e-146;		
Matches 300; Conservative	27;	Mismatches 18;	Indels 0;	Gaps 0;

[illegible]

Qy	121	GRMGSGVPEKQKSKGNHTRIRRVSDSEYPRPSEGFCHISHSIMPOVETTSVYLPPSS	180
Db	121	GRMGSGVPEKQKSKGNQIRIRVSDSEYPRPSEGFCHINHWMPQTEAVSPSYLPPSS	180
Qy	181	LSLDLLNNAVAFSSTLEELIRYLEPDPDMQVLDLSLYKPTMQLLGKAFVAGKSKRYVNLN	240
Db	181	LPDLDLNNATASSTLEDLIRYLEPEKMDLDLEDLYAPTMQLLGKAFVEGRKSRVVDNLN	240
Qy	241	LKEEVLKLYSCTPRNFSVISIREELKRTDTIFMPGCLLYKRCGGMCACCLHNCNECQCVPRK	300
Db	241	LTEEVRALYSCTPRNFSVISIREELKRTDTIFMPGCLLYKRCGGMCACCLHNCNECQCVPSK	300
Qy	301	VTKKKYHEVLDRPKTGVGKLYKSLTDVALEHNNEECDDCVGNNGG	345
Db	301	VTKKKYHEVLDRPKTGVGKLYKSLTDVALEHNNEECDDCVGNSTGG	345

RESULT 5
Q9NRA1

ID	Q9NRA1	PRELIMINARY;	PRT;	345	AA
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DT 01-OCT-2000 (TREMblrel). 15, Created)
DT 01-OCT-2000 (TREMblrel). 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel). 21, Last annotation update)
DE platelet-derived growth factor C.
DE

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RX MEDLINE=30268201; Pubmed=10806482;
 RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Uutela M.,
 RA Backstrom C., Hellstrom M., Bostrom H., Li H., Soriano P.,
 RA Besholtz C., Heldin C.-H., Allitalo K., Ostman A., Eriksson U.,
 RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
 receptor."

NC Natl. Cell Biol. 2:3025-3031(2000).
CC -1. SIMILARITY: CONTAINS 1 CUB DOMAIN
DR EMBL: AF244813; AAF80597.1; -
DR InterPro: IPRO000859; CUB domain.
DR InterPro: IPRO000072; PD_growth_factor
DR Pfam: PF004431; CUB: 1.
DR Pfam: PF00341; PDGF: 1.
DR SMART: SM00042; CUB: 1.
DR SMART: SM00141; PDGF: 1.
DR PROSITE: PSS0118; CUB: 1.
DR PROSITE: PSS0278; PDGF_2: 1.
SQ SEQUENCE 345 AA; 33043 MW; 5908896

Query Match	90.0%;	Score 1664;	DB 4;	Length 345;
Best Local Similarity	86.7%;	Pred. No. 1.5e+14;		
Matches 299;	Conservative 18;	Mismatches 0;	Gaps 0	

[illegible]

Db 241 LNEEYRLVSCPTPRNSVSIREELKRTDITFMPGCLLVKKRGCGNCAACCHNCGCCVPBK 300

Oy 301 YRKXHEVLQLRPKTGVKGSLKSFLDVAALEHHEBCDCVCGRNAG 345
|||||.....|||
Db 301 YRKXHEVLQLRPKTGVRLHKSLTDVALEHHEBCCVCRCSTGG 345

RESULT 6

ID O9I946 PRELIMINARY; PRT; 345 AA.

AC Q9I946;
Dr 01-OCT-2000 (TREMBREL_15, Created)
Dt 01-OCT-2000 (TREMBREL_15, last sequence update)
De 01-JUN-2002 (TREMBREL_21, last annotation update)

Dc Spinal cord-derived growth factor.
GN SCDF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

RN |||
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEHORIN; TISSUE=SPINAL CORD;
RX MEDLINE=20317014; PubMed=10856496;
RA Hamada T., Ut-Tel K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/YEGF family." ;
RL FEBS Lett. 475:97-102(2000) .
CC -! SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033829; BABO3265.1; CUB DOMAIN.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR00072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PSS0278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA99ZBF5J28C CRC64;

Query Match 84.0%; Score 1552; DB 13; Length 345;
Best Local Similarity 80.3%; Pred.No.3,4e-135;
Matches 277; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

Oy 1 MLTLGLLTLSLAGORTGTAEASNLSSKIQLSDSKRONGVOYPRIERYVTISNGSIHS 60
Db 1 MLLGLILLTSALAGRHHGAANEEDLSSEFPSPAKKEQGVDPQHCKITIIVTSGSIIHS 60

Oy 61 PRFRPHTPPNNMVLWMLAVADENVNRILTDEFRFGLEDPEDDICKDYFEVEEPDSGSYL 120
Db 61 PRFRPHTPPNTLYWLRLVAVDENVMIOLFDEFDFGLEPEDDICKYDFEVETPSDGTVL 120

Oy 121 GRMGCSGYVGKOTKSNIRIFUSDETFSEPSEGCIHYISTIMPOMETSPTSPSPSS 180
Db 121 GRWGSSSVYSPOIKSGNOAIRFYSEDTEFSQPGECHYTLLVPHNHHAESPSSLPSPA 180

Oy 181 LSIDLINNNAVFATFTLEELIRYLEPDPMOVDSLTYKPQTOLLGRAFIYGKRKSYVNLI 240
Db 181 LPDLVINNVAFESIVEELIRYLEPDRMDLDLEDLYLPWTOLLGKAYIHGRKSRVVDNI 240

Oy 241 LKEEKYLVISCPTPRNFVSIREELKRTDTIEWPGCLLVKRGCGNCAACCHNCGCCVPRK 300
Db 241 LKEEVRVLYSCPTRNFVSIREELKRTDTIEFWPLCLLVKRGCGNCAACHNCECCIPFK 300

Oy 301 YRKXHEVLQLRPKTGVKGSLKSFLDVAALEHHEBCDCVCGRNAG 345
Db 301 YRKXHEVLQLRPKTGVRLHKSLTDVALEHHEBCCVCRCSTGG 345

[illegible]

RA Hamada T., Ut-Fel K., Imaki J., Miyata Y.;
 RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
 SCDF/PDGF-C/fallotelin";
 RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-AORTA;
 RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
 Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
 Cao H.O., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
 Yuan U.G., Liew C.C., Zhao M.S., Hui R.T.;
 RN Submitted (Dec-1998) to the EMBL/genbank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-IRIS;
 RA Wistow G.;
 RT "Iris-expressed Growth Factor (IEGF).";
 RL Submitted (Feb-2001) to the EMBL/genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC PubMed-11331881;
 RA Bersten E., Rutela M., Li X., Pietras K., Ostman A., Heidin C.H.,
 Allitalo K., Eriksson U.;
 RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
 receptor";
 RL Nat. Cell Biol. 3:512-516(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-21231380; PubMed-11331882;
 RA LaRochele W.J., Jeffers M., McDonald W.F., Chiklaku R.A.,
 Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
 Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
 Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
 RT "PDGF D, A Novel Protease-Activated Growth Factor";
 RL Nat. Cell Biol. 3:517-521(2001).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; AB033832; BAB18903.1; -;
 DR EMBL; AF113216; AAG39287.1; -;
 DR EMBL; AY027517; AAK20081.1; -;
 DR EMBL; AF336376; AAK56136.1; -;
 DR EMBL; AF335584; AAK38840.1; -;
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR InterPro: IPR000531; TonB_boxc.
 DR Pfam: PF00431; CUB; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS50278; PDGF_2; 1.
 DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 DR SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674 CRC64;
 SQ

Query Match 40.7%; Score 752; DB 4; Length 370;
 Best Local Similarity 45.3%; Pred. No. 3,7e-61;
 Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;

QY 37 EONGVOD-PRHRYVITISNGSIHSPKPHPTPRNMVLYRLVAVDENRIQITFERG 95
 DB 42 ESNHLLDLYLRDRETTIOVKNGYVOSPRFNYSYRNLLTLWRHS-QENTRIQIVPNOG 100
 QY 96 LBDPEDDICKYFVEEPESDGSVL--GRWCGSGTVPKGOTSKGNHIRIRFVSDEYFPSE 153
 DB 101 LBEAENDICRYFVEVEDSETSTIIRGMCGHKEVPPRIKSTNOIKITFSDYFAVK 160
 QY 154 PGFCIHYSII--MPQVTEET-----SPSVLPSSLSLDLNNAYTAFST 195
 DB 161 PGFKIYISLLEDFOPAAASETWESVTSISGYSNPSVTPD-TLIDALDKIAEFD 219
 QY 196 LBEILRYLEPDMQVLDLSLYKPTWOLGKAFLYGKSKVYNLNLKEEVKLYSCTPRNF 255
 DB 220 VEDLLKYFPEWMOEDLENNYLDTPRYGRSY-HDRKSK-VLDRLINDDAKRYSCTPRY 277
 QY 256 SVSIREELKRTDTIWPGLLVKRCGCACCLHNCNCGCVPRKVTKKYHEVLQLRP-- 313

DB 278 SVNIREELKANVFPRLLYVRCGNGCGVTNMRSTCNSGKTVKKYHEVLQEPGH 337
 QY 314 -KTGVKGLKSLTDVALHNEHEDCYC 339
 DB 338 IKRRGAKTMAVLQIDHHERCDIC 364

RESULT 9
 ID Q9BWV5 PRELIMINARY; PRT; 364 AA.
 AC Q9BWV5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Iris-expressed growth factor short form.
 GN IEGF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-IRIS;
 RA Wistow G.;
 RT "Iris-expressed Growth Factor (IEGF).";
 RL Submitted (Feb-2001) to the EMBL/genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 CUB-DOMAIN.
 DR EMBL; AY027518; AAK20082.1; -;
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR000072; PD_growth_factor.
 DR InterPro: IPR000531; TonB_boxc.
 DR Pfam: PF00431; CUB; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00141; PDGF; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS50278; PDGF_2; 1.
 DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 DR SEQUENCE 364 AA; 42166 MW; 245C53E8DEA3EAC CRC64;
 SQ

Query Match 40.6%; Score 750.5; DB 4; Length 364;
 Best Local Similarity 45.6%; Pred. No. 4,9e-61;
 Matches 145; Conservative 58; Mismatches 86; Indels 27; Gaps 8;

QY 45 RHERVYITISNGSIHSPKPHPTPRNMVLYRLVAVDENRIQITFERGLEDPEDD 104
 DB 45 RDETIQVKGNGYVOSPRFNYSYRNLLTLWRHS-QENTRIQIVPNOGFGLEAENDIC 103
 QY 105 KYDFVEEPESDGSVL--GRWCGSGTVPKGOTSKGNHIRIRFVSDEYFPSEPGFCIHYST 162
 DB 104 RIDVEVEDSETSTIIRGMCGHKEVPPRIKSTNOIKITFSDYFAKPGFKIYISL 163
 QY 163 I--MPQVTEET-----SPSVLPSSLSLDLNNAYTAFSTLEELRYLE 204
 DB 164 LBDFOPAASETWESVTSISGYSNPSVTPD-TLIDALDKIAEFDYVLDLAKYTN 222
 QY 205 PDRMVDLSLYKPTWOLGKAFLYGKSKVYNLNLKEEVKLYSCTPRNFVSIREELK 264
 DB 223 PESWMOEDLENNYLDTPRYGRSY-HDRKSK-VLDRLINDDAKRYSCTPRYSVNIREELK 280
 QY 265 RDTITWPGCLLVKRCGCACCLHNCNCGCVPRKVTKKYHEVLQLRP--KTGVKGLH 321
 DB 281 LANVVEFPCLLVORCGNGCGVTNMRSTCNSGKTVKKYHEVLQEPGHIRRGRAKT 340
 QY 322 KSLTDVALHNEHEDCYC 339
 DB 341 MALVVDIQIDHHERCDIC 358

RESULT 10
 ID Q92517 PRELIMINARY; PRT; 370 AA.
 AC Q92517;

RC STRAIN=C57BL/6J; TISSUE=EMBRO.
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinaigawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., Kling B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Batsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarrelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Wilming L.,
RA wynshaw-booris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AK003359; BAB22735.1; -;
DR MGD: MGI:1919035; Pdfigd.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00431; CUB; 1.

DR SMART; SM00141; PDF, 1.
DR PROSITE; PS01180; CUB, 1.
DR PROSITE; PS50278; PDF_2; 1.

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Query Match      35.7%; Score 660; DB 11; Length 290;
Best Local Similarity 46.6%; Pred. No. 8,5e-53;
Matches 131; Conservative 48; Mismatches 76; Indels 26; Gaps
QY      82  ENVRITLPERFELEDPEDDICKYDFVEVEEEDSGS--VLGRMGCGSGTVPGKOTSKGNH 139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       7  EKTIOLESHQFLOFLAEFANDICRYDFVEVEESESSTVGRMGCGKKEIPITTSRTNO 66
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      140  IRIREFVDEVEFSPGPGICHSII---MPQVETLT-----SPSLVPPSSL 181
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       67  IKITFKSDDDFVAAPEGKTIYSFEVDFOFPAASFTNNESSTSGFSGVSYNSPITDP--TL 125
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      182  SLDLNNAAVTAFTLEELIRYLEBDRQVDDLISLYKPTWOLLRKAFLEGRKSKVYNLNL 241
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      126  TADVLDTVAEFEDVELDLKFNPNVSMODDLEMLYLTDPHYRGRSY-HDRKS-VLDRL 183
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      242  KEVEKLYSCGPRNVSYSIREELKRTDPIFMFGGLLYKRCGNGACCLHNNEGOCVPRRV 301
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      184  NDDVKRISCTPRNHSVNLREELKLITLNAVFPRCLLVLORCGNCGCGTVMKKSTCGSGKT 243
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      302  TKKYHVEQLDR---KTGVGLKSLTDVLAHHNEEDSCG 339
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 12
Q80FX6
AC Q80FX6; PRELIMINARY; .PRT; 923 AA.
DT 01-JUN-2002 (TREMBLrel. 2i, Created)
DT 01-JUN-2002 (TREMBLrel. 2i, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 2i, Last annotation update)
DE Neurophilin-1.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]_TAN
[1]

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CC -!- SIMILARITY: CONTAINS 5 CUB DOMAINS.
DR EMBL; D83476; BA01922.1; -.
DR HSSP; P00736; IAPQ.
DR MEROPS; M12.005; -.
DR InterPro; IPR001506; Astacin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR000130; Zn_MTpeptidase.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZMGC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 977 AA; 11019 MW; 4D7D2E37C64FDF1F CRC64;

Query Match 10.3%; Score 191; DB 13; Length 977;
Best Local Similarity 45.2%; Pred. No. 1e-08;
Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;

QY 55 NGSIHSKRPHTYPRNNVLVRLVAVDENVRIOQLTDFERFGLDEPDIDICKYDFVEVEE- 113
DB 590 NGSINSPGWPEKPPNNKNCIMQIVAPTO-YRISLKFDO--FETEGNDVCKYDFVEVRSG 645

QY 114 -PSDGSVLGRMGSGTVPKGTSGKNHRIREFVSDSEYFSPSPGF 156
DB 646 LTSDSKLHGKFCGS-ELPAVITSQYNNNRIFKSDNTV-SKGF 687

```

Search completed: April 29, 2003, 09:08:09
 Job time : 56 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 09:04:11 ; Search time 15.5 Seconds

(without alignments)
2139.766 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848

Sequence: 1 MLLGLLLLTSAAGQRTGT.....DVALHHECDVCVCRGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PTR_73:*

1: ptr1:*

2: ptr2:*

3: ptr3:*

4: ptr4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	754	40.8	370	2 JC7592	spinal cord-derivative
2	753	40.7	370	2 JC7591	spinal cord-derivative
3	191	10.3	707	2 JC2218	procollagen C-endo
4	190	10.3	823	1 A58788	procollagen C-endo
5	183.5	9.9	730	1 BMH01	procollagen C-endo
6	183.5	9.9	927	1 J00948	A5 antigen precursor
7	181	9.8	986	1 B58788	procollagen C-endo
8	181	9.8	991	2 I48540	procollagen C-endo
9	174.5	9.4	3623	2 T09456	intrinsic factor-B
10	160	8.7	3623	2 T08618	intrinsic factor-B
11	158	8.5	449	2 A55362	procollagen I C-pr
12	153	8.3	1057	1 A39288	dorsal-ventral pat
13	147.5	8.0	1524	2 T30337	polypeptide - Afri
14	145.5	7.9	686	1 A59271	Ra-reactive factor
15	144	7.8	699	1 I54763	Ra-reactive factor
16	143.5	7.7	597	2 S71352	metalloproteinase
17	141.5	7.7	1070	2 T31069	collagen-BMP-1 like
18	140.5	7.6	3871	2 T32812	hypothetical prote
19	139	7.5	1594	2 T30549	hensin - rabbit
20	137.5	7.4	705	1 C1HUR8	complement subcomp
21	135.5	7.3	1464	2 S58984	development protei
22	133.5	7.2	402	2 JH0403	procollagen I C-pr
23	128	6.9	277	2 A41735	hyaluronate-bindin
24	127	6.9	419	2 S69207	vascular endotheli
25	126.5	6.8	579	2 JCT629	membrane-type friz
26	125.5	6.8	245	1 TVCTSS	platelet-derived g
27	125.5	6.8	275	2 T30018	hypothetical prote
28	123	6.7	275	2 J06506	tumor necrosis fac
29	122.5	6.6	2403	2 A59386	sanko - human

30	119.5	6.5	2083	2 T42721	CRP-ductin-alpha p
31	117.5	6.4	276	2 A47290	TSG-6 homolog PS4
32	117.5	6.4	1290	2 A57190	ebnerin precursor
33	114.5	6.2	200	2 I51551	platelet-derived g
34	114.5	6.2	215	2 S08220	platelet-derived g
35	114.5	6.2	226	2 I51550	platelet-derived g
36	113	6.1	695	1 S05008	complement subcomp
37	112.5	6.1	241	1 PFH0G2	platelet-derived g
38	111.5	6.0	226	1 TVMVS5	PDGF-related trans
39	109	5.9	694	2 JC6554	complement subcomp
40	108.5	5.9	148	2 D49530	16k vascular endoc
41	107	5.8	321	2 T33161	hypothetical prote
42	104	5.6	319	2 I51569	UVS-2 protein - Af
43	103.5	5.6	225	2 S25097	platelet-derived g
44	103	5.6	196	2 B28964	platelet-derived g
45	103	5.6	211	1 PFH0G1	platelet-derived g

ALIGNMENTS

RESULT 1

JC7592

spinal cord-derived growth factor-B precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001

C:Accession: JC7592

R:Hamada, T., Uti-Tel, K., Imaki, J., Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A:Title: Molecular cloning of SCGF-B, a novel growth factor homologous to SCDF/PDGF

A:Reference number: JC7591; PMID:21092670; PMID:11162582

A:Contents: Fetal brain

A:Accession: JC7592

A:Molecule type: mRNA

A:Residues: 1-370 <HAM>

A:Cross-references: DDBJ:AB052170

C:Gene: scgfb

A:Gene: scgfb-B

F:1-17/Domain: secretory signal sequence #status predicted <SIG>

F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>

F:52-170/Region: CUB domain #status predicted

F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial g

F:294-308/Region: conserved motif #status predicted

Query Match 40.8%; Score 754; DB 2; Length 370;

Best Local Similarity 46.28; Pred. No. 1.4e-55;

Matches 151; Conservative 62; Mismatches 86; Indels 28; Gaps 10;

QY	37	EQNGVOD-PHREVRVITSGNGSHSPKFPHTYPRNMVLYVRLVAVDENVRITQTFDERFG	95
DB	42	ESNHLIDLYRDEINIRYTGHVOSPFEPNSYPRNLLITRLHS-QKTRIQALAFDHQFG	100
QY	96	LEDDPDDICKYDFEVEEPESDGS--VLGRWGSQTYVGKOTSGKNHIRIRFVSODEYPSE	153
DB	101	LEBAENDICRYDEVEEDVSESSYVGRWCGHKEIPRITSRTNQIKTFQSDPYVAK	160
QY	154	PGGCIHSHII---MPQ-----VRET-----TPSVLPSSSLDILNNAVTFST	195
DB	161	PGRIYISFEVDFQPEASAEIMESVTSFSGVSYHSPVW-DSTLADALDAIAEDFT	219
QY	196	LEELIRYLEPDRMOVDLSYKPTMOLLGKAFLYGKSKVYNLLEKEVYKLSCTPRNF	255
DB	220	VEDLTKTFNPMASODDLENLYMDTPRRGRSY-HERSK-VDDRLNDVYKRSCTPRNH	277
QY	256	SVSIREPLKRTDTIPFWDGCLLVKRCGNCACCLHNCNCCVPRKYKKYHEVQLRP--	313
DB	278	SVNDRLELKLITNAVFFPRCLLVORCGNCGGTLNMKSCSSGKTVKKYHEVLEKPRGH	337
QY	314	-KTVGKGLKSLDVALHHEHEDCVC 339	
DB	338	FKRRGKAKMALVDYIQDHHERCDCIC 364	

RESULT 2
JC7591
spinal cord-derived growth factor-B precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001
C:Accession: JC7591
R:Hameda, T.; U1-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDF-B, a novel growth factor homologous to SCDF/PDGF-C/
A:Reference number: JC7591; MUID:31092670; PMID:11162582
A:Accession: JC7591
A:Molecule type: DNA
A:Residues: 1-370 <HAM>
A:Cross-References: DDBJ:AB033832
C:Genetics:
A:Gene: scdgf-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth
F:294-308/Region: conserved motif #status predicted

[illegible]

RESULT 3
JC2218
procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
N/Alternate names: bone morphogenic protein 1
C/Species: *Xenopus laevis* (African clawed frog)
C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999
C/Accession: J02218
R/Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A/Title: Cloning and expression of cDNA encoding *Xenopus laevis* bone morphogenetic protein
A/Reference number: J02218; MUID:94085787; PMID:826384
A/Accession: J02218
A/Molecule type: mRNA
A/Residues: 1-707 <MAE>
A/Cross-references: GB:LI2249; NID:9406540; PIDN:AAA16313.1; PID:9406541
C/Comment: This protein induces ectopic cartilage formation in vivo.
C/Superfamily: procollagen C-endopeptidase; astracin homology; Clr/Clis repeat homology; E
C/Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
E:93-284/Domain: astracin homology <AST>
E:285-397/Region: complement I/r/Is-like repeat
E:285-394/Domain: Clr/Clis repeat homology <CLR1>
E:398-510/Region: complement I/r/Is-like repeat

```
F:398-507/Domain: C1r/C1s repeat homology <C1R2>
F:514-550/Domain: EGF homology <EGF>
E:554-666/Region: Complement I/LtS-like repeat
F:554-663/Domain: C1r/C1s repeat homology <C1R3>
F:62,105,295,326/Binding site: carboxylate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match          10.3%; Score 191; DB 2; Length 707;
Best Local Similarity 45.2%; Pred. No. 6,7e+08;
Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;
```

```
OY      55  NGSHTSPKPEPHPTPRNMYLVNRVAVDENVRLQLTDFDERFGLEDEDDICKDYFEVEE- 113
        |||::|||::| | | | | ::|||::| | | | | - :|||::|||
Db       562  NGSIINSPMPKEPYEPNKAKICIQWLVAPTQ-VYRIStLFDQ---FEETGNDVCKDYPEVRSG 617

OY     114  -PSDSGLGRMGSGTVPKGKTSKNHRIPIRPSEYPPEPGEF 156
        || | | | | | | | | | | | | | | | | | | | | | | | |
Db     618  LITSDSKLNGKFCGS-ELPAVVIITSQNNRNIRFKSDNTV-SKKGF 659
```

RESULT 4
A58788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
N:Alternate names: bone morphogenic protein splice form BMP-1/HIS
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
C:Accession: A37278; A58788
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mittleck, L.M.; Whitters, M.J.; Kriz, R.W.;
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702; 'EKRPALQPPRGKRPQHLKFRVQKRNTPQ' <MOZ>
A:Cross-references: GB:A422488; NID:g179499; PIDN:AAA51833.1; PID:g179500
J:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tollold homologue (mTld) are en
A:Reference number: A58788; MUID:95096114; PMID:7798260
A:Accession: A58788
A:Molecule type: mRNA
A:Residues: 703-823 <TAK>
A:Cross-references: GB:I35278; NID:g619423; PIDN:AAC41703.1; PID:g619424
C:Genetics:
A:Gene: GDB:BMP1, BMP-1
A:Cross-references: GDB:I125203; OMIM:112264
A:Map position: 8p21-8p21

[illegible]

Abstract: We have identified a candidate for the neuronal recognition molecule, nas homolog

E-322-431/Domains: C1r/C1s repeat homology <C1B1>
F-130-321/Domains: astacin homology <AST>
E-729-687/Locates: photoacrylate control line splice
F-130-321/Domains: astacin homology <AST>

F:435-544/Domain: C1r/C1s repeat homology <C1R2>

RESULT 7

B58788

procollagen C-endopeptidase (EC 3.4.24.13) precursor, collagen-like splice form - human

N|Alternate names: bone morphogenic protein 1, collagen-like splice form

C|Species: Homo sapiens (man)

C|Date: 28-Mar-1998 #sequence,revision 09-Apr-1998 #text,change 16-Jul-1999

C|Accession: A37278; B58788

R|Mozney, J.M.; Rosen, V.; Celeste, A.J.; Mltsock, L.M.; Whitters, M.J.; Kriz, R.W.;

Science 242, 1528-1534, 1998

A|Title: Novel regulators of bone formation: molecular clones and activities.

A|Reference number: A37278; MUID:89072730; PMID:3201241

A|Accession: A37278

A|Molecule type: mRNA

A|Residues: 1-702; 'EKRPALQPPGRGRHQLKRFVQRKRNTPQ' <MOZ>

A|Cross-references: GB:J22488; NID:g179499; PIDN:AAA51833.1; PID:g179500

R|Takahara, K.; Lyons, G.E.; Greenspan, D.S.

J. Biol. Chem. 269, 32572-32578, 1994

A|Title: Bone morphogenetic protein-1 and a mammalian collagen homologue (mTLD) are en-

A|Reference number: A58788; MUID:95096114; PMID:7798260

A|Accession: B58788

A|Molecule type: mRNA

A|Residues: 703-986 <TAK>

A|Cross-references: GB:J35279; NID:g619860; PIDN:AA041710.1; PID:g619861

C|Genetics:

A|Gene: GDB:BMP1; BMP-1

A|Cross-references: GDB:125203; OMIM:112264

A|Map position: 8p21-8p21

C|Function:

A|Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen t

C|Superfamily: procollagen C-endopeptidase; asclatin homology; C1r/C1s repeat homology; t

C|Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; <SIG>

F:1-32/Domain: signal sequence #status predicted <SIG>

F:23-986/Product: procollagen C-endopeptidase collagen-like splice form #status predicat

F:130-321/Domain: asclatin homology <AST>

F:332-431/Domain: C1r/C1s repeat homology <C1R1>

F:435-544/Domain: C1r/C1s repeat homology <C1R2>

Db 1089 HFTDFLEDFEGSCVDPEVI-RDGYE-TSPLVG---IV--CGSLVPTTISHSKML 1141
QY 249 -----SCTPRNFVSIRELKRRTDITFPGCLLVKRCGNCACCLHNCNCCVPRKYT 302
Db 1142 KFKSDAALAKGSA-----YWDGS--STGCGGN-----LTTPTGLVLSNYPM 1183
QY 303 KKYH---VLQLRPKTVKGLKSLTDVALEHHEEC 335
Db 1184 PYYHSECCYWRLEASHG-SPEFELEFQDFLEHHPSC 1218

RESULT 11
A53362
procollagen I C-proteinase enhancer protein precursor - human
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C:Accession: A53362
R:Rakshana, K.; Kessler, E.; Benjaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Shaw
J. Biol. Chem. 269, 26280-26285, 1994
A:Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, F
A:Reference number: A53362; MUID:95014462; PMID:7523404
A:Accession: A53362
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-449 <7AK>
A:Cross-references: GB:L33799; NID:6642907; PIDN:AAA61949.1; PID:6642908
C:Genetics:
A:Gene: GDB:PCOLCE
A:Cross-references: GDB:305468; OMIM:600270
A:Map position: 7q21.3-7q22
C:Superfamily: Clr/Cls repeat homology
C:Keywords: extracellular protein; glycoprotein; pyroglutamic acid
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-449/Product: #status predicted <MAT>
F:37-146/Domain: Clr/Cls repeat homology <CLR1>
F:159-270/Domain: Clr/Cls repeat homology <CLR2>
F:26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:29,431/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.5%; Score 158; DB 2; Length 449;
Best Local Similarity 34.5%; Pred. No. 2.2e-05;
Matches 48; Conservative 21; Mismatches 50; Indels 20; Gaps 9;

QY 56 GSISHSPKPHRT-YPRNMVLVRLVAVDENVRQLTFDEREGLEDPEDDICKYDFVEV--- 111
Db 168 GTLTTFNVEDSDVPPGISCSWHIAPDQV-IALTF-EKRDLE--PDYCRVSVSVFNG 223
QY 112 EEPDGSVLGRMGSGTVPEKQTSKGNHRIKRVSDPEPSEPCIHYSIM----- 164
Db 224 AVSDSRRLKKEFGCD-AVPGSISSEGNELVCFVSDLSVAD-GFSASYTLPRGTAKEG 281
QY 165 --PQVETTSPPSY-LPSS 180
Db 282 QGPGPKRGTEPKVKLPKPS 300

RESULT 12
A39288
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A39288
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A:Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone
A:Reference number: A39288; MUID:92034970; PMID:1840509
A:Accession: A39288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1057 <SHI>
A:Cross-references: GB:M76976; NID:9157305; PIDN:AAA28491.1; PID:9157306
C:Genetics:
A:Gene: FlyBase:tlid

A:Cross-references: FlyBase:FBgn0003719
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; Clr/Cls r
C:Keywords: duplication; hydrolase; metalloproteinase; zinc
F:136-329/Domain: astacin homology <AST>
F:352-464/Domain: Clr/Cls repeat homology <CLR1>
F:468-578/Domain: Clr/Cls repeat homology <CLR1>
F:585-620/Domain: EGF homology <EG1>
F:624-740/Domain: Clr/Cls repeat homology <CLR3>
F:747-782/Domain: EGF homology <EG2>
F:787-896/Domain: Clr/Cls repeat homology <CLR4>
F:900-1013/Domain: Clr/Cls repeat homology <CLR5>
F:221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted
F:222/Active site: Glu #status predicted

Query Match 8.3%; Score 153; DB 1; Length 1057;
Best Local Similarity 33.3%; Pred. No. 0.00018;
Matches 47; Conservative 28; Mismatches 54; Indels 12; Gaps 7;

QY 13 LAGQRTGTRAESNLSSKQLQSDKEQNGVQDPKHERV---VTISGNGSIHSPKPHYTP 68
Db 432 VSGEVITTTQSRMLNVNNAKGRGFK-ARFEVCGGDLTKFDQSIDSPNPMYDM 490
QY 69 RNMVLVRLVAVDENVRQLTFDEREGLEDPEDDICKYDFVEV--PDSGVLGRMGCS 126
Db 491 PDECVWRITAPD-NHQVALKF-QSFELE--KHDGCAVDFEIRDSNHSRILGRFGCD 546
QY 127 GTVPKQTSKGNHRIKRVESD 147
Db 547 KLPPNIRKT-RSNQYIRFVSD 566

RESULT 13
T30337
polyprotein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T30337
R:Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A:Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from
A:Reference number: Z20829
A:Accession: T30337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1524 <YAN>
A:Cross-references: EMBL:081290; NID:g2981640; PID:g2981641; PIDN:AAC24717.1

Query Match 8.0%; Score 147.5; DB 2; Length 1524;
Best Local Similarity 28.7%; Pred. No. 0.00082;
Matches 54; Conservative 34; Mismatches 73; Indels 27; Gaps 10;

QY 56 GSISHSPKPHRTYPRNMVLVRLVAVDENVRQLTFDEREGLEDPEDDICKYDFVEV-EEP 114
Db 439 GMITSPPYDPYPRRLKTCNV-IIEAPENHIVKLKFEF-FVVEYGHG--CIYDAVEYDGA 494
QY 115 SDGSVLGRMGSGTVPEKQTSKGNHRIKRVSDPEPSEPCIHYSIMPO-----VT 168
Db 495 EEKQILARLCGY-TLPLPISSPENTMLIRKTD-MENSYGFKVKSFSVKEKQFSLPVD 552
QY 169 ETTSPVLPSSLSLDLNNV-VTAFSTLEELRYLEPP-----RMOVDL-----DS 214
Db 553 DLTPTISMLHRAIALDVCNAMPTKMWLPRIVYGGEEASNSMPWQQLFLLTFHCEGA 612
QY 215 LYKPTWQL 222
Db 613 IISPMWL 620

RESULT 14
A59271
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 08:58:01 ; Search time 9 Seconds
(without alignments)
1589.926 Million cell updates/sec

Title: US-09-818-943-2

Perfect score: 1848
Sequence: 1 MULTICLUSTALAGORTGT.....DVALEHHECDCVCRGNAGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	10.3	707	1	BMPL_XENLA
2	183.5	9.9	928	1	NRPL_XENLA
3	181	9.8	986	1	BMPL_HUMAN
4	181	9.8	991	1	BMPL_MOUSE
5	176	9.5	923	1	NRPL_HUMAN
6	174	9.4	1022	1	TLD_BRARE
7	172	9.3	922	1	NRPL_RAT
8	169	9.1	923	1	NRPL_MOUSE
9	167	9.0	914	1	NRPL_CHICK
10	163.5	8.8	616	1	SPAN_STRPU
11	158	8.5	449	1	PCOI_HUMAN
12	155.5	8.4	925	1	NRPL_MOUSE
13	155.5	8.4	931	1	NRPL_RAT
14	155.5	8.4	931	1	NRPL_MOUSE
15	153.5	8.3	326	1	VEGD_RAT
16	153	8.3	1057	1	TLD_DROME
17	147.5	8.0	704	1	CRAR_MOUSE
18	145.5	7.9	686	1	MAST_HUMAN
19	144.5	7.8	597	1	BP10_PARLI
20	144	7.8	699	1	CRAR_HUMAN
21	137.5	7.4	705	1	CIR_HUMAN
22	136.5	7.4	468	1	PCOI_RAT
23	136	7.4	354	1	VEGD_HUMAN
24	135.5	7.3	358	1	VEGD_MOUSE
25	133.5	7.2	468	1	PCOI_MOUSE
26	132	7.1	415	1	VEGD_MOUSE
27	130	7.0	639	1	BMPL_STRPU
28	128	6.9	277	1	TS6G_HUMAN
29	127	6.9	419	1	VEGD_HUMAN
30	125.5	6.8	419	1	PDGB_FELCA
31	123	6.7	275	1	TS6G_MOUSE
32	117.5	6.4	276	1	TS6G_RABIT
33	114.5	6.2	226	1	PDGA_XENLA

34	113	6.1	695	1	CASP_MESAU
35	112.5	6.1	241	1	PDGB_HUMAN
36	111.5	6.0	164	1	VEGA_CAVPO
37	111.5	6.0	226	1	TSIS_SMSAV
38	109	5.9	855	1	ST14_HUMAN
39	108.5	5.9	148	1	VEGD_ORFN7
40	105.5	5.7	207	1	VEGD_HUMAN
41	104	5.6	514	1	UVS2_XENLA
42	103.5	5.6	207	1	VEGD_BOVIN
43	103.5	5.6	225	1	PDGB_RAT
44	103.5	5.6	241	1	PDGB_SHEEP
45	103	5.6	211	1	PDGA_HUMAN

ALIGNMENTS

```

RESULT 1
BMPL_XENLA
ID BMPL_XENLA STANDARD: PRT; 707 AA.
AC P98070;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=94085787; PubMed=8262384;
RX Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
RT Cloning and expression of cDNA encoding Xenopus laevis bone
RT morphogenetic protein-1 during early embryonic development."
RL Gene 134:257-261(1993).
CC - FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER
CC - DIFFERENTIATION OF DEVELOPING ORGANS.
CC - DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED
CC - TADPOLES; LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTRULA.
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
CC - SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC - SIMILARITY: CONTAINS 3 CUB DOMAINS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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-----
CC EMBL: L12249; AAA16313.1; -
CC HSSP: P00736; IAP0.
CC MEROPS: M12.005.-
DR InterPro: IPR001506; Astacin.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000130; zn_MTPptase.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00431; CUB; 3.
DR Pfam: PF01400; Astacin; 1.
DR PRINTS: PR00480; ASTACIN.
DR SMART: SM00042; CUB; 3.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00235; ZNMG; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR PROSITE: PS01180; CUB; 3.
DR PROSITE: PS001010; ASX_HYDROXYL; 1.

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```

DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA_1.
KW Growth factor: Cytokine; Repeat: Bone; Cartilage; Hydrolase; Protease;
KW Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein.
FT SIGNAL 1 ? POTENTIAL.
FT PROPEP 83 ? POTENTIAL.
FT CHAIN 84 707 BONE MORPHOGENETIC PROTEIN 1.
FT DOMAIN 84 284 METALLOPROTEASE.
FT DOMAIN 285 397 CUB 1.
FT DOMAIN 398 509 CUB 2.
FT DOMAIN 510 551 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 554 666 ZINC 3.
FT METAL 176 176 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 177 177 BY SIMILARITY.
FT METAL 180 180 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 186 186 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 514 526 BY SIMILARITY.
FT DISULFID 522 535 BY SIMILARITY.
FT CARBOHYD 537 550 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 707 AA; 80673 MW; 1B6980D716DC98BD CRC64;

Query Match 10.3%; Score 191; DB 1; Length 707;
Best Local Similarity 45.2%; Pred. No. 5; 1e-08;
Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;

QY 55 NGSIHSPKPHRYPRNMVLVRLVAVDENVRQLTDFPERGLEDPEDDICKYFVEE- 113
DB 562 NGSIHSPGKPEHPKNCNCTQVLVAPQ-YRISLKDQ---PETEGNDVCKYDVEVRSG 617
QY 114 -PSDGSVLGRMGSGTVPGKOTSGKNHRIKRVSDYEPSEPGF 156
DB 618 LTFSDSKLHGKFGCS-ELPAVITSGYNNMRLEPKSDNTV-SKKGF 659

RESULT 2
ID NRPL_XENLA STANDARD; PRT; 928 AA.
AC P28824;
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neutropilin-1 precursor (A5 protein) (A5 antigen).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91337458; PubMed=1908252;
RT Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
RT The A5 antigen, a candidate for the neuronal recognition molecule,
RT has homologues to complement components and coagulation factors.*;
RL Neuron 7:295-307(1991).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CEREBRAL NEURONAL CIRCUITS AND IN ORGANOREGULATION OF THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY
CC SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION
CC BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER
CC NEURONS.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.

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CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: D10467; BAA01260.1; -
CC HSSP: P12259; 1CZT.
CC InterPro: IPR000859; CUB_domain.
CC InterPro: IPR000421; F5F8_C.
CC InterPro: IPR000998; MAM_domain.
CC Pfam: PF00431; CUB_2.
CC Pfam: PF00629; MAM_1.
CC Pfam: PF00754; F5_F8_Type_C_2.
CC PRINTS: PR00020; MAMDOMAIN.
CC SMART: SM00042; CUB_2.
CC SMART: SM00331; FAS8C_2.
CC SMART: SM00137; MAM_1.
CC PROSITE: PS00740; MAM_1; 1.
CC PROSITE: PS01180; CUB_2.
CC PROSITE: PS01285; FAS8C_1; 2.
CC PROSITE: PS01286; FAS8C_2; 2.
DR PROSITE: PS50060; MAM_2; 1.
KW Transmembrane; Glycoprotein; Neuron; Signal; Repeat; Receptor;
KW Antigen.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 928 NEUROPILIN-1.
FT DOMAIN 22 860 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 861 880 POTENTIAL.
FT DOMAIN 884 928 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 584 F5/8 TYPE C 2.
FT DOMAIN 646 812 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 584 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 844 844 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 928 AA; 103416 MW; AFB323B0A4CT89D CRC64;

Query Match 9.9%; Score 183.5; DB 1; Length 928;
Best Local Similarity 30.7%; Pred. No. 2; 9e-07;
Matches 55; Conservative 34; Mismatches 65; Indels 25; Gaps 9;

QY 50 VTIHSGNSIHSKPHRYPRNMVLVRLVAVDENVRQLTDFPERGLEDPEDDICKYDFV 109
DB 31 KITSPSYLTSAGIPSPYSQRCENLQAPDEHYRIMNFHFDEDEH---CRYDIV 87
QY 110 EV--EERPSDGSVLGRMGSGTVPGKOTSGKNHRIKRVSDYEPSEPGFCHYSIIM--P 165
DB 88 EVIDGDANANQLGKCYCK-IAISPLVSTGPSIFIRVSDYEPFG-AGFSIRYEVKTGP 145
QY 166 QVTE--TTSQVLP-----PSSLSLDLNNAVTAFTLEELRYLEPDRMQVDLS 214
DB 146 ECSRNFSSNGIKSPKPYPEKYNALCTYIIFA---PKMQEIV--LEEFSEFLDADS 198

RESULT 3
ID BMP1_HUMAN STANDARD; PRT; 986 AA.

```


DB 660 L7ADSKLHGKFCGS-EKPEVITSQYNNMRYEKFSDMTV-SKNGKFAHF 705

RESULT 5

NRPI_HUMAN STANDARD: PRT; 923 AA.

ID NRPI_HUMAN 060461;

AC 014786; 060461;

DT 30-MAY-2000 (Rel. 39, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Neutrophilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).

GN NRPI OR NRP OR VEGF165R.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RA [1] SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM).

RX MEDLINE=97433084; PubMed=9288753;

RT He Z., Tessier-Lavigne M.,

RT "Neutrophilin is a receptor for the axonal chemorepellent semaphorin III."

RT Cell 90:739-751(1997).

RL [2] SEQUENCE FROM N.A. (MEMBRANE-BOUND ISOFORM), AND SEQUENCE OF 22-39.

RN TISSUE-Breast;

RP MEDLINE=98188099; PubMed=9529250;

RC Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.,

RA "Neutrophilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.";

RT Cell 92:735-745(1998).

RL [3] SEQUENCE FROM N.A. (SOLUBLE/SNRPI ISOFORM), AND SEQUENCE OF 22-31.

RP TISSUE-Prostatic adenocarcinoma;

RC MEDLINE=20183929; PubMed=10688880;

RA Gagnon M.L., Bieleberg D.R., Gschltman Z., Miao H.-Q., Takashima S., Soker S., Klagsbrun M.,

RT "Identification of a natural soluble neutrophilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor activity."

RT Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).

RL [4] CHARACTERIZATION.

RP MEDLINE=20309748; PubMed=10748121;

RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.,

RT "Neutrophilin-2 and neutrophilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of Placenta growth factor-2, but only neutrophilin-2 functions as a receptor for the 145-amino acid form of VEGF."

RT J. Biol. Chem. 275:18040-18045(2000).

RL -1- FUNCTION: THE MEMBRANE-BOUND ISOFORM IS A RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOPUSANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165 ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS.

CC -1- FUNCTION: THE SOLUBLE/SNRPI ISOFORM BINDS VEGF-165 AND APPEARS TO INHIBIT ITS BINDING TO CELLS. IT MAY ALSO INDUCE APOPTOSIS BY SEQUESTERING VEGF-165. MAY BIND AS WELL VARIOUS MEMBERS OF THE SEMAPHORIN FAMILY. ITS EXPRESSION HAS AN AVERSE EFFECT ON BLOOD VESSEL NUMBER AND INTEGRITY.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SOLUBLE/SNRPI ISOFORM IS SECRETED.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: MEMBRANE-BOUND (SHOWN HERE) AND SOLUBLE/SNRPI. ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: THE EXPRESSION OF MEMBRANE-BOUND AND SOLUBLE/SNRPI ISOFORMS DOES NOT SEEM TO OVERLAP. THE MEMBRANE-BOUND ISOFORM IS EXPRESSED BY THE BLOOD VESSELS OF DIFFERENT

CC TISSUES. IN THE DEVELOPING EMBRYO IT IS FOUND PREDOMINANTLY IN THE NERVOUS SYSTEM. IN ADULT TISSUES, IT IS HIGHLY EXPRESSED IN HEART AND PLACENTA. MODERATELY IN LUNG, LIVER, SKELETAL MUSCLE, KIDNEY AND PANCREAS; AND LOW IN ADULT BRAIN. THE SOLUBLE/SNRPI ISOFORM IS FOUND IN LIVER HEPATOCYTES, KIDNEY DISTAL AND PROXIMAL TUBULES.

CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.

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CC -----

CC EMBL: AF018956; AAC51759.1; -

CC EMBL: AF016050; AAC12921.1; -

CC EMBL: AF145712; AAF4344.1; -

CC HSSP: P12259; 1CZT.

CC GeneW: HGNC:8004; NRPI.

CC MIM: 602069; -

CC InterPro: IPR000859; CUB_domain.

CC InterPro: IPR000421; FAS5_C.

CC InterPro: IPR001092; HLH_Basic.

CC InterPro: IPR000998; MAM_domain.

CC Pfam: PF00431; CUB; 2.

CC Pfam: PF00629; MAM; 1.

CC Pfam: PF00754; F5_F8_type_C; 2.

CC PRINTS: PR00020; MAMDOMAIN.

CC SMART: SM00042; CUB; 2.

CC SMART: SM00231; FAS5C; 2.

CC SMART: SM00137; MAM; 1.

CC PROSITE: PS01180; CUB; 2.

CC PROSITE: PS01285; FAS5C_1; 2.

CC PROSITE: PS01286; FAS5C_2; 2.

CC PROSITE: PS00740; MAM_1; 1.

CC PROSITE: PS00600; MAM_2; 1.

CC Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;

CC Alternative splicing.

CC FT SIGNAL 1 21

CC FT CHAIN 1 923

CC FT DOMAIN 22 856

CC FT TRANSMEM 857 879

CC FT DOMAIN 923 923

CC FT DOMAIN 27 141

CC FT DOMAIN 147 265

CC FT DOMAIN 275 424

CC FT DOMAIN 431 583

CC FT DOMAIN 645 811

CC FT DISULFID 27 54

CC FT DISULFID 82 104

CC FT DISULFID 147 173

CC FT DISULFID 206 228

CC FT DISULFID 275 424

CC FT DISULFID 431 583

CC FT CARBOHYD 150 150

CC FT CARBOHYD 261 261

CC FT CARBOHYD 300 300

CC FT CARBOHYD 522 522

CC FT CARBOHYD 842 842

CC FT VARSPLC 642 644

CC FT VARSPLC 645 923

CC FT CONFLICT 26 26

CC FT CONFLICT 749 749

CC FT CONFLICT 855 855

CC FT SEQUENCE 923 AA; 103120 MW; ADEADCA4A95ED57 CAC64;

Query Match 9.5%; Score 176; DB 1; Length 923;

Best Local Similarity 32.6%; Pred. No. 1,2e-06;

Matches 57; Conservative 24; Mismatches 68; Indels 26; Gaps 9;

FT	DOMAIN	645	811	MAM.	PROBABE.
FT	DISULFID	27	54		PROBABE.
FT	DISULFID	82	104		PROBABE.
FT	DISULFID	147	173		PROBABE.
FT	DISULFID	206	228		PROBABE.
FT	DISULFID	275	424		BY SIMILARITY.
FT	DISULFID	431	583		BY SIMILARITY.
FT	CARBOHYD	150	150		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	261	261		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	300	300		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	522	522		N-LINKED (GLCNAC. . .)
FT	CARBOHYD	841	841		N-LINKED (GLCNAC. . .)
SO	SEQUENCE	922 AA;	103082 MM;	CC6F82AD098B0F2E	CRC64;
Query Match		9.38;	Score 172;	DB 1;	Length 922;
Best Local Similarity		31.58;	Pred. No. 2.5e-06;		
Matches	56;	Conservative	21;	Mismatches	67;
				Indels	34;
				Gaps	8;
Qy	2	LILGLILTLTSLALACQRTSTRAESNLSKLTQSLSDKEQNGVDPFRHERVVTISGNSIHSP	61		
Db	7	LILCATLALALALAG-----AFRSKDCGG-----TILKIEINPEYLSP	42		
Qy	62	KEPHTYPPNNMVLVMBLVAVDENVRIGLTLPDERBFGLEDPEDDICKYDPEV--EEDSDGSV	119		
Db	43	GYPHSYHSEKCEWMLIQAPPEYQRTIMNFPHFLEDRD---CKDYAVEVIDGENEGRL	99		
Qy	120	LGRMGSGTGVGKQTSKCNHRIREFSDVEYFSESGFCIHYSIIM--POVET-NSPS	174		
Db	100	WGKEGK-IASPVVSSPFLFKVSD-YETHGAGFSIRIEIFRKGEGSCSNTYAPT	155		
RESULT 8					
NRPI_MOUSE					
ID	NRPI_MOUSE	STANDARD;	PRT;	923 AA.	
AC	P97333:				
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Neurophilin-1 precursor (A5 protein).				
GN	NRPI OR NRP.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/C; TISSUE=Embryonic brain;				
RX	MEDLINE=96353149; PubMed=8748368;				
RA	Karakami A., Kitesukawa T., Takagi S., Fujisawa H.				
RT	"Developmentally regulated expression of a cell surface protein,				
RL	neurophilin, in the mouse nervous system.";				
RL	J. Neurobiol. 29:1-17(1996).				
CC	-1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE				
CC	CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF				
CC	CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS				
CC	SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT				
CC	BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165				
CC	ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN				
CC	INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.				
CC	IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- TISSUE SPECIFICITY: NERVOUS SYSTM.				
CC	-1- SIMILARITY: BELONGS TO THE NEUROPHILIN FAMILY.				
CC	-1- SIMILARITY: CONTAINS 2 CUB DOMAINS.				
CC	-1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.				
CC	-1- SIMILARITY: CONTAINS 1 MAM DOMAIN.				
CC	-----				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/)				

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CC or send an email to license@slb.ch).
CC -----
CC EMBL: D50086; BAA08789.1; -.
CC HSSP: P12259; ICZT.
CC MGD: MGI:106206; Nrp.
CC InterPro: IPR000859; CUB_domain.
CC InterPro: IPR000421; FA58_C.
CC InterPro: IPR000998; MAM_domain.
CC Pfam: PF00431; CUB; 2.
CC Pfam: PF00629; MAM; 1.
CC Pfam: PF00754; F5_F8_type_C; 2.
CC SMART: SM00042; CUB; 2.
CC SMART: SM00231; FA58C; 2.
CC SMART: SM00137; MAM; 1.
CC PROSITE: PS01180; CUB; 2.
CC PROSITE: PS01285; FA58C_1; 2.
CC PROSITE: PS01286; FA58C_2; 2.
CC PROSITE: PS00740; MAM_1; 1.
CC PROSITE: PS50060; MAM_2; 1.
CC Transmembrane; Glycoprotein;
KW SIGNAL 1 21
FT CHAIN 22 923 NEUROFILIN-1.
FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 857 879 POTENTIAL.
FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 583 F5/8 TYPE C 2.
FT DOMAIN 645 811 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 842 842 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 923 AA; 103020 MW; 0644BBA170796808 CRC64;

Query Match 9.1%; Score 169; DB 1; Length 923;
Best Local Similarity 31.5%; Pred. No. 4.5e-06;
Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;

OY 2 LLLGLLLLSALAGGRTGRTAESNLSSKLOLSDKEONGVQDRHREYVITSGNGSIHSP 61
DB 7 LCATLALALALAG-----AFRSDKCGG-----TIKENPGYLTP 42
OY 62 KPFTYPRNVLVWRVAVDENYRIQLTDERGLDEPDICKYDFVEV--EPPSDGSV 119
DB 43 GYHSHYPSKCMWLOAPRYORIIINRPHDLDRD---CKDYVEYIDENEGRL 99
OY 120 LGHWGSGTVPGKQTSKGNHRIREVSDEYFSPGFCIHYSTIM--PQYLET-TSPS 174
DB 100 WGFCKCK-IAPSPVSSGPFLLFIKFWSD-YETHGAGFSIKYEIKFGKPECSQNYTAPT 155

RESULT 9
ID NRPI_CHICK STANDARD; PRT; 914 AA.
AC P79795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurofilin-1 precursor (A5 protein).
GN NRPI OR NRP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

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OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Embryonic brain;
RX MEDLINE=95324761; PubMed=7601310;
RA Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsudoi M., Kawakami A.,
RA Fujisawa H.;
RT "Expression of a cell adhesion molecule, neurofilin, in the
RT developing chick nervous system.";
RL Dev. Biol. 170:207-222(1995).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY
CC SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
CC PROPERTIES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM
CC (LAYERS D AND E OF GSEs), AMACRINE CELLS OF RETINA, NEURITES OF
CC DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, E.G.
CC BLOOD VESSELS IN THE ENTIRE EMBRYO.
CC -1- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC -----
DR EMBL: DA5416; BAA08256.1; -.
DR HSSP: P12259; ICZT.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00629; MAM; 1.
DR Pfam: PF00754; F5_F8_type_C; 2.
DR PRINTS: PR00020; MAMDOMAIN.
DR SMART: SM00042; CUB; 2.
DR SMART: SM00231; FA58C; 2.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS01285; FA58C_1; 2.
DR PROSITE: PS01286; FA58C_2; 2.
DR PROSITE: PS00740; MAM_1; 1.
DR PROSITE: PS50060; MAM_2; 1.
DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
KW Cell adhesion.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 914 NEUROFILIN-1.
FT DOMAIN 20 847 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 848 870 POTENTIAL.
FT DOMAIN 871 914 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 139 CUB 1.
FT DOMAIN 145 263 CUB 2.
FT DOMAIN 273 422 F5/8 TYPE C 1.
FT DOMAIN 429 581 F5/8 TYPE C 2.
FT DOMAIN 636 801 MAM.
FT DISULFID 25 52 PROBABLE.
FT DISULFID 80 102 PROBABLE.
FT DISULFID 145 171 PROBABLE.
FT DISULFID 204 226 PROBABLE.
FT DISULFID 273 422 BY SIMILARITY.
FT DISULFID 429 581 BY SIMILARITY.
SQ SEQUENCE 914 AA; 102480 MW; DD2EBDD6FCBB68C CRC64;

Query Match 9.0%; Score 167; DB 1; Length 914;
Best Local Similarity 28.8%; Pred. No. 6.4e-06;

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RL Cell Struct. Funct. 21:662-662(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99018118; PubMed-9799793;
 RA Gloeckner G., Scherer S., Schatkevoy R., Boright A., Weber J.,
 RA Tsui L.-C., Rosenthal A.;
 RT "Large-scale sequencing of two regions in human chromosome 7q22:
 RT analysis of 650 kb of genomic sequence around the EPO and CUGT1 loci
 RT reveals 17 genes";
 RL Genome Res. 8:1060-1073(1998).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-99134301; PubMed-9933570;
 RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;
 RT "Structural organization and expression patterns of the human and
 RT mouse genes for the type I procollagen COOH-terminal proteinase
 RT enhancer protein";
 RL Genomics 55:229-234(1999).
 RN [6]
 RP PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
 RX MEDLINE-20092917; PubMed-10625689;
 RA Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,
 RA Banda M.J.;
 RT "Post-translational proteolytic processing of procollagen C-terminal
 RT proteinase enhancer releases a metalloproteinase inhibitor";
 RL J. Biol. Chem. 275:1384-1390(2000).
 CC -1- FUNCTION: BINDS TO THE COOH-TERMINAL PROPEPTIDE OF TYPE I
 CC PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.
 CC -1- FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE AN
 CC METALLOPROTEINASE INHIBITORY ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 NTR DOMAIN.
 CC -----
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 CC -----
 CC DR EMBL, L33799; AAA61949.1; ALT_SEQ.
 CC DR EMBL, AB008549; BAA23281.1; -
 CC DR EMBL, AF053355; AAC78800.1; -
 CC DR EMBL, AF083655; AAD16041.1; -
 CC DR GeneW, HGNC:8738; PCOLCE.
 CC DR MIM, 600270; -
 CC DR InterPro: IPR000859; CUB_domain.
 CC DR InterPro: IPR001134; Netrin_C.
 CC DR Pfam: PF00431; CUB; 2.
 CC DR Pfam: PF01759; NTR; 1.
 CC DR SMART, SM00042; CUB; 2.
 CC DR PROSITE, PS01180; CUB; 2.
 CC DR Glycoprotein; Repeat; Signal.
 CC FT SIGNAL 1 25 POTENTIAL.
 CC FT CHAIN 26 449 PROTEIN.
 CC FT DOMAIN 37 149 CUB 1.
 CC FT DOMAIN 159 273 CUB 2.
 CC FT SITE 287 288 NTR.
 CC FT SITE 288 289 CLEAVAGE.
 CC FT SITE 293 294 CLEAVAGE.
 CC FT SITE 299 300 CLEAVAGE.
 CC FT SITE 303 304 CLEAVAGE.
 CC FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 449 AA: 47972 MW: 3D88430158648796 CR64;
 Query Match 8.5%; Score 158; DB 1; Length 449;

Best Local Similarity 34.5%; Pred. No. 1.5e-05;
 Matches 48; Conservative 21; Mismatches 50; Indels 20; Gaps 9;
 QY 56 GSHSKRFPHF-IPRMVWLVRLVAVDENVRIQITFDERGLDEPDDICKYFVEY--- 111
 Db 168 GLLTPMPWPSDYPGIRSCWHIAPPDV-IALTP-EKEDL--PDYCRYSVSFNG 223
 QY 112 EEPDSDSLGRMGSGTVPKQTSKGNHRIKRVSPDEYFSEPGFCHVSIIM----- 164
 Db 224 AVSDDSRLRLKFCGD-AVPSGISSEGNELLVQVPSDLSYAD-GFSASKYLTPRTAKES 281
 QY 165 --PQVETTSVSV-LPPSS 180
 Db 282 QCGPKRGTEPEPKVLPKPS 300
 RESULT 12
 NRP2_RAT
 ID NRP2_RAT STANDARD; PRT; 925 AA.
 AC 035276;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropilin-2 precursor (vascular endothelial cell growth factor 165
 DE receptor 2).
 GN NRP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley;
 RX MEDLINE-97433085; PubMed-9288754;
 RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tal Y.-T., Giger R.J.,
 RA Ginty D.D.;
 RT "Neuropilin is a semaphorin III receptor";
 RL Cell 90:753-762(1997).
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
 CC AND VEGF-145 ISOMERS OF VEGF. AND THE PLGF-2 ISOMER OF PGF.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE
 CC CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE
 CC LINING IN THE RIBS.
 CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
 CC -----
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 CC -----
 CC DR EMBL, AF016297; AAC53338.1; -
 CC DR HSP, P12259; ICF2.
 CC DR InterPro: IPR000859; CUB_domain.
 CC DR InterPro: IPR000421; FA58_C.
 CC DR InterPro: IPR000998; MAM_domain.
 CC DR Pfam: PF00431; CUB; 2.
 CC DR Pfam: PF00629; MAM; 1.
 CC DR Pfam: PF00754; F5_F8_type_C; 2.
 CC DR SMART, SM00042; CUB; 2.
 CC DR SMART, SM00231; FA58C; 2.
 CC DR SMART, SM00137; MAM; 1.
 CC DR PROSITE, PS01180; CUB; 2.
 CC DR PROSITE, PS01285; FA58C_1; 2.
 CC DR PROSITE, PS01286; FA58C_2; 2.
 CC DR PROSITE, PS50060; MAM_2; 1.
 CC DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.

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FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 925 NEUROFILIN-2.
FT DOMAIN 23 858 EXTRACELLULAR (POTENTIAL).
FT TRASMEN 859 883 POTENTIAL.
FT DOMAIN 884 925 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 142 CUB 1.
FT DOMAIN 149 267 CUB 2.
FT DOMAIN 277 427 F5/8 TYPE C 1.
FT DOMAIN 434 592 F5/8 TYPE C 2.
FT DOMAIN 642 802 MAM.
FT DISULFID 28 55 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 833 833 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 925 AA; 103896 MM; 3BF62903F644851C CRC64;

Query Match 8.4%; Score 155.5; DB 1; Length 925;
Best Local Similarity 33.3%; Pred. No. 5.7e-05;
Matches 41; Conservative 19; Mismatches 56; Indels 7; Gaps 4;

OY 42 ODPHRRVYVTSNGSISHPKPHPTPRNVVLMRLVAVDENRIQLTPDERGLEPED 101
DB 24 ODPCCGKSKDAGYITSPGYPODIPSHONCEWVYAPAPNOKIYVLFNPHIEIENHD 82
OY 102 DICKEYFVEVEEPDS--VLGRMGCSGYVPGKOTSKGNHIRIRFVSEDFEPSEPCIH 159
DB 83 --CKYPIEIRDDSDSADLLGKHGNC-IAPPTIISGSVLYIKFTSD-YAROGAGSLR 138
OY 160 YST 162
DB 139 YET 141

RESULT 13
NR22_HUMAN STANDARD; PRT; 931 AA.
ID NR22_HUMAN 014820; 014821;
AC 060462; 014820; 014821;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Neurofilin-2 precursor (Vascular endothelial cell growth factor 165
DE receptor 2).
GN NRP2 OR VEGF165R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A0 AND A17).
RX MEDLINE-97470888; PubMed-931348;
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
RT "Neurofilin-2, a novel member of the neurofilin family, is a high
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema
RT III."
RL Neuron 19:547-559(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A22).
RC TISSUE-Breast;
RX MEDLINE-98188099; PubMed-9529250;
RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;
RT "Neurofilin-1 is expressed by endothelial and tumor cells as an
RT isoform-specific receptor for vascular endothelial growth factor."
RL Cell 92:735-745(1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE-20309748; PubMed-10748121;

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RA gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
RT "Neurofilin-2 and neurofilin-1 are receptors for the 165-amino acid
RT form of vascular endothelial growth factor (VEGF) and of placenta
RT growth factor-2, but only neurofilin-2 functions as a receptor for
RT the 145-amino acid form of VEGF."
RL J. Biol. Chem. 275:18040-18045(2000).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3E, VEGF-165
CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC -1- SUBUNIT: NEUROFILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
CC NEUROFILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A22 (SHOWN HERE), A0 AND A17;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -----
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CC -----
DR EMBL: AF022859; AAC51788.1; -
DR EMBL: AF022860; AAC51789.1; -
DR EMBL: AF016098; AAC12922.1; -
DR HSSP: P12259; ICZT.
DR Genev: HGNC:8005; NRP2.
DR MIM: 602070; -.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000421; FA58_C.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00629; MAM; 1.
DR Pfam: PF00754; F5_F8_Type-C; 2.
DR SMART: SM00042; CUB; 2.
DR SMART: SM00231; FA58C; 2.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS01285; FA58C_1; 2.
DR PROSITE: PS01286; FA58C_2; 2.
DR PROSITE: PS50060; MAM_2; 1.
KW Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
KW Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 931
FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).
FT TRASMEN 865 889 POTENTIAL.
FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 142 CUB 1.
FT DOMAIN 149 267 CUB 2.
FT DOMAIN 277 427 F5/8 TYPE C 1.
FT DOMAIN 434 592 F5/8 TYPE C 2.
FT DOMAIN 642 802 MAM.
FT DOMAIN 671 674 POLY-SER.
FT DISULFID 28 55 BY SIMILARITY.
FT DISULFID 83 105 BY SIMILARITY.
FT DISULFID 149 175 BY SIMILARITY.
FT DISULFID 208 230 BY SIMILARITY.
FT DISULFID 277 427 BY SIMILARITY.
FT DISULFID 434 592 BY SIMILARITY.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 833 839 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 809 813 MISSING (IN ISOFORM A17).
FT VARSPIC 809 830 MISSING (IN ISOFORM A0).
FT CONFLICT 602 602 E -> K (IN REF. 1).
SO SEQUENCE 931 AA; 104830 MM; 270CBAE69A0A97C CRC64;

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ID VEGD_RAT STANDARD: PRT: 326 AA.
AC 035251;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE growth factor) (rgef).
GN FIGF OR VEGFD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Yamada Y., Hirata Y., Nezu J., Shimane M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -i- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC and endothelial cell growth, stimulating their proliferation and
CC migration and also has effects on the permeability of blood
CC vessels. May function in the formation of the venous and lymphatic
CC vascular systems during embryogenesis, and also in the maintenance
CC of differentiated lymphatic endothelium in adults. Binds and
CC activates VEGFR-3 (Flt4) receptor (By similarity).
CC -i- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
CC -i- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -i- PTM: Undergoes a complex proteolytic maturation which generates a
CC variety of processed secreted forms with increased activity toward
CC VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC linked by disulfide bonds before secretion. The fully processed
CC VEGF-D is composed mostly of two VEGF homology domains (VHDS)
CC bound by non-covalent interactions (By similarity).
CC -i- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
CC EMBL: AF014827; AAB66557.1; -.
CC DR HSSP: P15692; 1VPP.
CC DR InterPro: IPR004153; CXCCX_repeat.
CC DR InterPro: IPR000072; PD_growth_factor.
CC DR Pfam: PF00341; PDGF_1.
CC DR Pfam: PF03128; CXCCX; 1.
CC DR ProDom: PD001629; PD_growth_factor; 1.
CC DR SMART: SM00141; PDGF_1.
CC DR PROSITE: PS00249; PDGF_1; 1.
CC DR PROSITE: PS50278; PDGF_2; 1.
CC KM Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
CC cleavage on pair of basic residues; Multigene family.
CC FT SIGNAL 1 21
CC FT PROPEP 22 93
CC FT CHAIN 94 210
CC FT PROPEP 211 326
CC FT DOMAIN 227 317
CC FT REPEAT 227 242
CC FT REPEAT 263 278
CC FT REPEAT 282 298
CC FT REPEAT 306 317
CC FT DISULFID 116 158
CC FT DISULFID 147 194
CC FT DISULFID 151 196
CC FT DISULFID 141 141
CC FT DISULFID 150 150
CC FT CARBOHYD 160 160
CC FT CARBOHYD 190 190
CC FT CARBOHYD 292 292
CC FT CARBOHYD 326 AA; 37112 MW; 1261AFA373596C00 CRC64;
CC SEQUENCE

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Query Match      8.3%; Score 153.5; DB 1; Length 326;
Best Local Similarity 27.7%; Pred. No. 2.3e-05;
Matches 56; Conservative 28; Mismatches 81; Indels 37; Gaps 9;

QY 155 GFCIHYSITMPQVTEHTSPSVLPSPSSISLDLNNAVASTLEELIRYLEPDRWY---- 210
      ||| : : : ||| | : : ||| ||| : : ||| ||| : : |||
Db 21 GFSIEHRAVAVDSILERSRSRLERS-----EQQIRASTLEELLQVAHSEDMKLMRCR 73

QY 211 -----DLSLYKPTWQLLGRAFLYGGKSKVYNLNLKEVLYSGTPNFSVSIREE 263
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 74 LKLSLANDSRSTSHRSTREAFTEYDET---LVVIDEWORTQCSPRETCVEVASL 129

QY 264 -KRTDTIFMPGCLLYKRCGNCACCLHNCNCCVPRK--VTKKYHEVLQLRPKTVKVG 319
      | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 130 CKTTNTPFKRPPCVNVRCCG---CC--NEBSVCMNTSTYISKQLFEISV--PLTSV-- 180

QY 320 LKSLTDVALEHHEEDCCVCRG 341
      | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 181 -PELVPVKRIANHTGCKCLPTG 200

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Search completed: April 29, 2003, 09:06:15
Job time : 13 secs

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